STIC-Biot ch/Ch mLib

Fr m: Sent:

Davis, Minh-Tam

To:

Monday, September 16, 2002 9:58 AM STIC-Biotech/ChemLib Search request for 09/802520

Subject:

Please search in commercial database and in issued patent files: Oligomer search for SEQ ID NO:3-9.

Thank you.
MINH TAM DAVIS
ART UNIT 1642, ROOM 8A01, MB 8E12
305-2008

Edward Hart

Technicai Info. Specialist

STIC/Biotech

CMI 6B02 Tel: 305-9203

portey data 3/01

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
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Lexis/Nexis:
Sequence Sys.: _(DO
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us-09-802-520-9.rst

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: szhaoétigg.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.biffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tbb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI: Site_2: EcoRI: Female C57BL/65 mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size
                                                                                                                                 Mus musculus
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 183)
  RPCI-23-17L22.TV RPCI-23 Mus musculus genomic clone RPCI-23-17L22,
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                             Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
Contact: Shaying Zhao Contact: Shaying Zhao Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Pel: 301 838 0200
Fax: 301 838 0200
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Mismatches
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E 1 (bases 1 to 184)

S Malek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizi,B., Pertea,G.,
Sultana,R., Taai,J., White,J., Quackenbush,J. and Lee,N.H.
Generation of ESTS from Normalized Rat Embryo, Bento Soares
L Unpublished (2000)
Cother_ESTS: ESTS13021
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-3529
Exa: (301)-838-5209
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="mixed tissue"
/lab_host="DHS-alpha"
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/note="PH7"
/note PR3TPPA"
Combination of Rov, RBR, RKI, RLI, RPL, RLU, REM, RMU, RSP
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RCORI: Site_2: EcoRI; Female C57BL/67 mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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Homo sapiens genomic DNA, 21q region, clone: 762015N19, genomic
Action (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/Dac_ends/mouse/Dac_end_intro.html
Plate: 384 row: I column: 12
Seg primer: SP6
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Submitted (23-SEP-1998) to the DDBJ/EWBL/GenBank databases.
Masahira Hattori, Kitasato University, Department of Science, JST
Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan
(E-mail:hattori@hqc.ims.u-tokyo.ac.jp, Tel:0427-78-9732,
Fax:0427-78-9561)
On Feb 6, 1999 this sequence version replaced gi:2992368.
AG006490: Submitted (77-Mar-1998).
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Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published only in DataBase (1998) In press
2 (bases 1 to 723)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
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/db_xref="taxon:9606"
/chromosome="21"
/clone="762015N19"
                                                                                                                                                                                   /organism-"Mus musculus"
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Clones are derived from the rat BAC library CHORI-230
Clones are derived from the rat BAC library
(http://www.chori.org/bacpac/rat230.htm). For BAC library
avallability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/note="Vector: pTARBAC2.1; Site_1: EcoR1; Site_2: EcoR1;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
                                                                                         Gaps
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Pred. No. 12;
); Mismatches 0; Indels
7.9%; Score 21; DB 12; Length 723; 100.0%; Pred. No. 4.1; 1.1ve 0; Mismatches 0; Indels
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/db_xref="texon:10116"
/clone="CH230-2A16"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
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        Query Match 7.9
Best Local Similarity 100.
Matches 21; Conservative
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Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                 Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 87 row; C column: 1
Seq primer: SP6
Class: BAC ends.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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Contact: Robert B. Welss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
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Pred. No. 4.1;
0; Mismatches 0; Indels
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-87C1"
/clone_lib="RPCI-23"
/sex="Female"
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100.0%; Pre
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Fax: 801 585 7177
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// And June 1. Coll Strain All Volue, in Tresistant, for And June 1. Coll Strain All Volue, in Tresistant, for And June 1. Coll Strain All Volue, in Tresistant, for Male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gl14732114)plAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 721)
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Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pleter de Jong
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 0208
Plate: 0049 row: M column: 16
Seep primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 614.
                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                      /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0049M16"
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Best Local Similarity 100.(
Matches 21; Conservative
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AQ529197.1 GI:4841310
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/db_xref="G1:12836271"
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LESPRIEITSYLGLHHGSGQFFHDVEVEDVLDPSCKRSPSTATLHLPSLEAYRDPSCLS
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
14. .2125
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                                                     Please visit our web site (http://genome.gsc.riken.go.jp/) for
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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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/organism="Mus musculus"
/strain="C57BL/G1"
/db_xref="MGD:MGI:1904359"
/db_xref="taxon:10090"
/clone="1200016E19"
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1184 c 964
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/note="putative"
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AZZ4ZDZ1 SS 15-JUN-2000 PRCI-23-87C1,TJ RPCI-23 Mus musculus genomic clone RPCI-23-87C1,
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Mus.
Lases 1 to 557)

Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSS: RPCI-23-87CI.TV
                                                                                                                                                                                                                                                                                                                                                                                                        Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pleter de Jong

(pieter@dejong med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:

Rttp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seg primer: SPG class: BAC ends.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                 Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /ceil_type="Lymphocytes"
/note="Vector: pBACe3"; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
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                                                                                                                                                                     Unpublished (1997)
Other (5Ss: RPCI-11-367B5.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
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/db_xref="taxon:9606"
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100.0%; Pre
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                                                  (bases 1 to 357
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168 ttttcttcaagttaattttcac 189
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     δλ
             /strain="c78L", day musculus / strain="c78L", day xref="taxon:10090" / c1one="UI-W-AO1-aej-d-05-0-UI" / clone="UI-W-AO1-aej-d-05-0-UI" / clone="UI-W-AO1-aej-d-05-0-UI" / clone="UI-W-AO1-aej-d-05" / dev_stage="17-32 days" 
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Hattori,M., Ishli,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q

L Published Only in DataBase (1998) In press

E (bases 1 to 729)

Hattori,M., Ishli,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Blitcet Submission

L Damitted (23-SEP-1998) to the DDBJ/EMBL/GenBank databases.

Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattoriehgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9551)

On Feb 6, 1999 this sequence version replaced gi:2992367.
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Homo sapiens genomic DNA, 21q region, clone: 762015N19, genomic
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.2;
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/organism="Mus musculus"
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/db_xref="taxon:9606"
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AG014774.1 GI:3649992
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Functional annotation of a full-length mouse cDNA collection
In Nature 409, 685-690 (2001)
E 5 (bases 1 to 4077)
S Adachi, J. Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,
Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,
Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiranda, T., Horin, F.,
Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S.,
Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,
Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Schimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Togami, M., Tagawa, A., Takahashi, F.,
Tanaka, T., Tejlma, Y., Toya, T., Yamamura, T., Yamanaka, I.,
Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                               AKO04810 4077 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200016E19:nuclear factor of activated T-cells, cytoplasmic 1, full insert sequence.
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Ronno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected CDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (strain:C57BL/6J) adult male lung cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:1200016E19.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
415 TTTTCTTCAAGTTAATTTTCAC 436
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AK004810.1 GI:12836270
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1.8 ug of total RNA, treated with TA DNA polymerase, and purified by ethanol-precipitation. The copys were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDMAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and centricon 100. The cDMAs were digested with Sal1 and NoII enzymes and cloned into Sal1/NoII site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.4 kb. The library was constructed by Yulan Piao (NIA).
       Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
                            a long-transcript enriched CDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Double-stranded CDNAs were synthesized with an Oligo(dT) primer
                                                                                                                               ch 9.4%; Score 25; DB 10; Length 585; l Similarity 100.0%; Pred. No. 0.036; 25; Conservative 0; Mismatches 0; Indels
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Tel: 301 443 1706
Fax: 301 443 9890
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Plao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Pantano, S., Luo, A. and Ko, M.S.H.
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada Tel: 780 492 0169
Tel: 780 492 4068
Email: smoore@afns.ualberta.ca
Insert Length: 558 Std Error: 0.00
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Ridge/Mesonephros cDNA Library (Long)
L Unpublished (2001)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
33 Cassell Dirtye, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0927 row: C column: 09
Seq primer: -21M13 Forward
High quality sequence stop: 585
POLYA=Yes.
                                                                                                                                                                                                                     /db_xref="taxon:9913"
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/tclone_lib="Bos taurus Duodenum #1 library"
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/cell_type="Simple columnar epithelial"
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/dev_stage="Young adult"
/lab_host="XLI-BlueMRF'strain"
/note="Organ: Intestine/duodenum; Vector: Uni-2ZAPXR;
/note="Organ: Site_2: Xho I"
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/dev_stage="12.5-dpc"
/lab_host="DH10B"
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/sex="Male"
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/organism="Mus musculus"
/strain="c5TBL/G1"
/db_xref="niaEST:C0927C09-3"
/db_xref="taxon:10090"
/clone="C0927C09"
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AI845434 11-05-0-UI.sl NIH_BMAP_MPG_N Mus musculus CDNA clone UI-M-AOl-aej-d-05-0-UI.sl NIH_BMAP_MPG_N Mus musculus CDNA clone UI-M-AOl-aej-d-05-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                              Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 385)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mESTemail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized pineal glands library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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Computer-based methods for the mouse full-length cDNA
Y. and Hayashizaki, Y.
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BM431438
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SOURCE
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                                       /dev_stage="Addit"
//dev_stage="Addit"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Akimura, T. Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatau, N., Hiramcto, K., Hiracka, T., Hirozane, T., Imotani, K., Ishii,
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akhaira, S., Tanaka, T., Tomaru, A., Toya, T.,
Natahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (10 (11), Trylunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
peres. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Tonoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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100.0%; Pred. No. 9.90
**ve 0; Mismatches
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50 c 42 g 1
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/db_xref="taxon:9606"
                       /clone_lib="CT0510'
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BB691606.1 GI:16018339
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B. -RNA was provided by Akira Nakagawara, DIV. of Blochemistry, Chiba Cancer Center Research Institute, 666-2 Nitona, Chuoh-ku, Chiba, 260-8717 Japan, whose assistance we gratefully acknowledge."
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     ō
                                                                                                                                                                                                                                                                                    /clone="7120429L21"
/clone_lib="RIKEN full-length enriched, 2 days neonate
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Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E., Sensen,C.W., Gordon,P.W.K. and Moore,S.S.
Gene Expression Profilling of the Bovine Gastrointestinal Tract
encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="sympathetic ganglion"
/dev_stage="2 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
0.035;
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Pred. No. 0.03
0; Mismatches
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Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
                                                                                                                                                                                                    /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                sympathetic ganglion"
/sex="mixed"
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Best Local Similarity 100.0%; Pi
Matches 25; Conservative 0;
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7.5 325 9 BB550302 7.5 356 9 BB562468 7.5 397 9 A1061309 7.5 398 12 AQ42494 7.5 415 9 AW241285 7.5 423 10 T85142 7.5 429 12 AQ037959 7.5 429 12 AQ037959 7.5 431 9 AW836404	20 7.5 456 12 B94936 B94936 CIT-HSP-216 20 7.5 473 12 BH039744 BH30944 BH30935 CIT-HSP-216 20 7.5 483 12 AQ209876 H930935 CH2124-3 20 7.5 504 10 W03237 BH309325 CH230-LB 20 7.5 541 9 AA755962 V73609 R73569 V736412 20 7.5 561 10 BG791810 BG79180 V736412 R755962 V736412 20 7.5 563 10 BG694791 BG6994791 BG6994791 BG6994791 BG6994791	BF336378 BF36378 BF36	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2-CM3-CT0510- 010900-319-c09&t3=2000-09-01&t4-1) Seq primer: puc 18 forward High quality sequence start: 3 High quality sequence stop: 359. Location/Qualifiers ce l. 359 //organism="Homo sapiens"
00 0 000	00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 BF336378/C LOCUS DEFINITION ACCESSION VERSION KEYWORS SOURCE ORGANISM REFERENCE AUTHORS JOURNAL MEDLINE	COMMENT COMMENT FEATURES SOUTCE
4.5 Compugen Ltd. s Search time 5053.42 Seconds (without alignments) (w	tatgttttgttttgttttgc	results predicted by chance to have a . to the score of the result being printed, of the total score distribution. SUMMARIES ID	BF33678 CM3-CT051 BB691606 BB691606 BM431438 IDM016F03 BM219592 C0927C09- A1845434 UI-M-A01- AG014774 HOMO Sapi AK004810 MMS MWSCU AG029197 RPCI-11-3 AZ242621 RPCI-23-8 AZ34261 RPCI-23-8 AZ04261 RPCI-23-8 AZ04261 RPCI-23-8 AZ018110 RPCI-23-3 AG014775 HOMO Sapi BE199080 EST455471 BF29080 EST455471 BF29080 EST455471 BM418291 BM418291
GenCore version 4 Copyright (c) 1993 - 2000 C OM nucleic - nucleic search, using sw model Run on: September 20, 2002, 08:33:58	Title: Derfect score: 265 Sequence: 1 ccggagaggggcacagtaat Scoring table: Gapop 60.0 , Gapext 60.0 Searched: 13736207 seqs, 6748477542 residu Word size: 0 Total number of hits satisfying chosen parameters Minimum DB seq length: 0 Maximum DB seq length: 0 Maximum DB seq length: 2000000000	EST:* : em_estba:* 2: em_estbum:* 3: em_estin:* 4: em_estin:* 5: em_estoy:* 6: em_estoy:* 7: em_estpl:* 7: em_estpl:* 10: qb_estl:* 11: qb_htc:* 11: qb_htc:* 11: qb_htc:* 11: qb_htc:* 11: qb_ntc:* 11: em_gss_ln:* 12: qb_ns:* 13: em_gss_ln:* 14: em_gss_ln:* 15: em_gss_ln:* 16: em_gss_ln:* 16: em_gss_ln:* 17: em_gss_ln:* 18: em_gss_ln:* 18: em_gss_ln:* 19: em_gss_ln:* 10:	C 1 63 23.8 359 10 BF336378 4 25 9.4 500 9 BB691606 4 25 9.4 500 9 BB691606 5 22 8.3 385 9 A1845434 5 22 8.3 385 9 A1845434 C 7 22 8.3 729 12 AG014774 C 8 21 7.9 357 12 AG014774 C 10 21 7.9 557 12 AZ242621 C 11 21 7.9 557 12 AZ242621 C 13 20 7.5 149 12 BAZ16190 C 14 20 7.5 189 12 BAZ16190 C 15 20 7.5 189 12 BAZ16190 C 15 20 7.5 189 12 BAZ16190 C 16 20 7.5 184 10 BF290880 C 17 20 7.5 181 12 AZ21142 C 17 20 7.5 184 10 BF290880

Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bruice, Thomas C.
APPLICANT: ATA, Dev P.
TITLE OF INVENTION: DECXYNUCLEIC ALKYL THIOUREA COMPOUNDS AND USES THEREOF;
FILE REFERENCE: 30448.65US02
CURRENT APPLICATION NUMBER: US/09/407,675
CURRENT FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/091,481
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/111,800
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1998-12-11
SPRIOR APPLICATION NUMBER: 60/111,800
PRIOR FILING DATE: 1998-12-11
SOFTWARE: PALENTING DATE: 1998-12-11
SOFTWARE: PALENTING DATE: 2.0
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                                                                                                                                                                                               Length 18;
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00.0%; Pred. No. 16;
.ve. 0; Mismatches (
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Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches
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                                                                                                                                                                                                      100.08; Pre-
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; Sequence 2, Application US/09407675
; Patent No. 6169176
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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                                        LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: singl
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Best Local Similarity
Matches 17; Conserva
                                                                                                              linear
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TOPOLOGY:
US-09-106-038A-83
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100.0%; Pred. No. 3.4;
tive 0; Mismatches 0; Indels 0
                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
ATORNEY/AGENT INFORMATION:
NAME: FILIX, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 01/957-000100
TELEPHONE: 415-576-0200
TELEPHONE: 415-576-0300
INFORMATION FOR SED ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 83, Application US/09106038A
Patent No. 6007995
GENERAL INFORMATION:
APPLICATURE OF INVENTION: ANTISENSE MODULATION OF THERI
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Isis Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Isis Pharmaceuticals, Inc. 2292 Faraday Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Laurel Spear Bernstein
REGISTRATION NUMBER: 37.280
REFERENCE/DOCKET NUMBER: RTS-0004
TELECHONE: (760) 931-9200
TELEPHONE: (760) 603-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,038A
FILING DATE: June 26, 1998
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.8'
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: no'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-106-038A-83/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-724-394A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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Fatent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Lauer, Peter M.
APPLICANT: Huddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF SEQUENCES: 31
CORRESONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó;
   APPLICANT: Thomas, Winston
APPLICANT: Tsuchhashi, Zenta
APPLICANT: Tsuchhashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STARFE: CAN ADDRESSED ADDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%; Score 18; DB 2; Length 246240;
100.0%; Pred. No. 3.4;
tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA

ZIP: 94111-3834

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTONEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
REGISTRATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION THE SY6-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | NAME/KEY: misc_feature
| LOCATION: 1..246240
| OTHER INFORMATION: /note= "HLA-H.CONTIG"
| US-08-724-394A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.8%
Best Local Similarity 100.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: not rele
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                                                                                                                                                                                                                                                                                                                                                                                 CA
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US-08-724-394A-22
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                                                                                                                                                                                              Sequence 20. Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: USA
ZIP: 9411-3834
ZIP: 9411-3834
ZUP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATE: PATENTION DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION: NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
FREGISTRATION NUMBER: 017957-000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
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Sequence 21, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 0179
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: not relevant TOPOLOGY: not relevant
2316 TGTTTGTTTGTTTGC 2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 1..246240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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RESULT 12

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Gaps

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APPLICANT: HOUDEBINE, Louis-Marie
APPLICANT: DEVINOY, Eve
APPLICANT: THEPOT, Dominique
TITLE OF INVENTION: Production of a Protein of Interest in
TITLE OF INVENTION: the Milk of a Transgenic Mammalian
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.8%; Score 18; DB 4; Length 4157; 100.0%; Pred. No. 4.1; ve 0; Mismatches 0; Indels
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                    join(1868..1949, 2462..2587, 2888..3046, 3416
                                                                                                                    Length 4157
                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,127
                                                                                                                  6.8%; Score 18; DB 2;
100.0%; Pred. No. 4.1;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/07179
FILING DATE: 12-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,146
                                                                                                                                                                                                                                                                                                 RESULT 10
US-09-314-127-2
; Sequence 2, Application US/09314127
; Patent No. 6268545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08; Pro
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TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                       2316 TGTTTGTTTTGTTTTGC 2333
                                                                                                                                                                                                  248 tgttttgttttgtttgc 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 tgttttgttttgttttgc 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4157 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                    Query Match 6.8°
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: WEGNER, Harold C
REGISTRATION NUMBER: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.8°
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                         ..3429)
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                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
  ; NAME/KEY:
; LOCATION:
; LOCATION:
US-08-162-146-2
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; LOCATION:
US-09-314-127-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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APPLICANT: HOUDEBINE, Louis-Marie
APPLICANT: DEVINOY, Eve
APPLICANT: THEFOT, Dominque
TITLE OF INVENTION: Production of a Protein of Interest in
TITLE OF INVENTION: the Milk of a Transgenic Mammalian
NUMBER OF SEQUENCES:
ADDRESSED: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                          Length 2688;
                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,146
FILING DATE: 10-FEB-1994
                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                      6.8%; Score 18; DB 100.0%; Pred. No. 4.2 ative 0; Mismatches
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FF92/00533
FILING DATE: 12-JUN-1992
PRIOR APPLICATION NUMBER: FR 91/07179
FILING DATE: 12-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGISTRATION NUMBER: 25,258
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                          by experiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08162146 Patent No. 5965788
                    CDNA to mRNA
                                                                                                                                                                                , 2004-10N: 1042 ..., 199
; LOCATION: 2105 to 2269
; LOCATION: 2370 to 2462
; IDENTIFICATION METHOD: by
US-08-909-965C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202) 672-5300
(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                    248 tgttttgttttgttttgc 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                           951 TGTTTTGTTTTGC 968
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 4157 base pairs
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                         358 to 486
560 to 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3000 K SI
CITY: Washington
STATE: D.C.
                                                       UNGANISM: human
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
TOPOLOGY: line
MOLECULE TYPE: c
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                         LOCATION:
LOCATION:
                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-162-146-2
                                                                                                  CLONE:
                                                                                                                                                                                                                                                                                                                                          Query Match
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NAME/KEY: primer_bind

LOCATION: 1897..1917

OTHER INFORMATION: /label= primer6044-5

OTHER INFORMATION: /note= "annealing of primer 6044-5 (table 4) to

GHER INFORMATION: amplify subfragments (opposite strand)"

US-09-117-927-4
                          primer 6044-3 (table 4) to
                                                                                                                                                                             primer 6044-4 (table 4) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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4.2;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,965C
FILING DATE: August 12, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DF 322745/95
APPLICATION NUMBER: DF 322745/95
FILING DATE: 12-No. 5936078-1995
FILING DATE: 12-No. 5936078-1995
ATTOMEEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Kuga Tetsro
APPLICANT: Nakagawa Satoshi
APPLICANT: Sakaki yoshiyuki
APPLICANT: Zhao Nanding
APPLICANT: Hashida Hideji
TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE
TITLE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: FITZPATRICK, CELLA, HARPER AND SCINTO STREET: 277 Park Avenue CITY: New York
OTHER INFORMATION: /label= primer6044-3
OTHER INFORMATION: /note="annealing of pri
OTHER INFORMATION: amplify subfragments"
NAME/KRY: primer_bind
LOCATION: 1918..1940
OTHER INFORMATION: /label= primer6044-4
OTHER INFORMATION: /note="annealing of pri
OTHER INFORMATION: amplify subfragments"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.8%; Score 18; DB 100.0%; Pred. No. 4.2 Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
CONNTRY: U.S.A.
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: ISM PC COMPATIBLE
COMPUTER: ON TYPE: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08909965C Patent No. 5936078
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TELECOMMUNICATION INFORMATION
TELEPHONE: 212-758-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 236262
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawrence S. Perry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212-758-2982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-909-965C-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME:
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LOCATION: 2128..2163
OTHER INFORMATION: /note= "Sequence of pMOG553
Patent No. 626334
OTHER INFORMATION: upstream (5') of the uid A translation initiation
OTHER INFORMATION: codon up to the RB/plant genome transition."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: primer_bind
LOCATION: 1147..1169
OTHER INFORMATION: /label= primer6044-2
OTHER INFORMATION: /note= "annealing of primer 6044-2 (table 4) to
OTHER INFORMATION: amplify subfragments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "annealing of primer 6044-1 (table 4) to amplify subfragment"
APPLICANT: OHL, Stephan Andreas
APPLICANT: SIJMONS, Peter Christian
APPLICANT: SIJMONS, Peter Christian
APPLICANT: VAN DER LEE, Frederique Marianne
APPLICANT: KLAP, Joke Johannes Maria
APPLICANT: KLAP, Joke Johanna Catharina
TITLE OF INVENTION: NEMATODE-INDUCIBLE PLANT GENE PROMOTER
WUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                 ZITE: NX
ZITE: NX
ZITE: NX
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" FLOPPY disk
COMPUTER: LBM PC compatible
COMPUTER: LBM PC compatible
COMPUTER: WANDENFERECT 8
SOFTWARE: WANDENFERECT 8
FLING DATE: WANDENFERECT 8
FLING DATE: 26-APR-1996
FLING DATE: 26-APR-1996
FLING DATE: APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MASS, CLIFFORD J.
FREIERRENCE/DOCKET NUMBER: U-012011-9
TELEFANICATION INFORMATION:
TELEFANICATION INFORMATION:
TELEFANICATION INFORMATION:
TELEFANICATION INFORMATION:
TELEFANICATION OF 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2163 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= primer6044-1
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LOCATION: 2161..2163
OTHER INFORMATION: /codon_start= 2161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO ONG STREET SOURCE: ORGANISM: Arabidopsis thaliana STRAIN: C24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                     1: LADAS & PARRY 26 WEST 61 STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: primer_bind
LOCATION: 787..804
OTHER INFORMATION: /la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: promoter LOCATION: 1.2127
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OTHER INFORMATION:
                                                                                                                                                                                                                                                       CITY: NEW YORK
                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
FEATURE:
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Gaps
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APPLICANT: Hirano, Toshio
APPLICANT: Akira, Shizuo
APPLICANT: Tanabe, Osamu
APPLICANT: Tanabe, Osamu
APPLICANT: Kinoshita, Shiqemi
APPLICANT: Kinoshita, Shiqemi
APPLICANT: Shimmonto, Takuya
TITLE OF INVENTION: C/EBP2 Gene and Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.8%; Score 18; DB 1;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sughrue, Mion, Zinn, Macpeak
ADDRESSEE: Seas
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
STATE: D.C.
COUNTRY: United States
LIP: 20037-3203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,735
FILING DATE: 1993023
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION INFORMATION:
TELEFONMUMICATION INFORMATION:
TELEFONMUMICATION INFORMATION:
TELEFONMUMICATION STATES
INFORMATION FOR SEG ID NO: 1:
                                                                                                                                                         Sequence 1, Application US/08012735 Patent No. 5360894 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Sequence 4, Application US/09117927
; Patent No. 6262344
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                                1752 ATGTTTTGTTTTGTTTTG 1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1752 ATGTTTTGTTTTG 1769
             247 atgttttgttttgttttg 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 atgttttgttttgttttg 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1914 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEIC ACID
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 281..1316
; OTHER INFORMATION:
US-08-012-735-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                   US-08-012-735-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-117-927-4
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                                                                                                                                                                                                                    6.8%; Score 18; DB 4; Length 1910;
100.0%; Pred. No. 4.2;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.8%; Score 18; DB 1; Length 1914; Best Local Similarity 100.0%; Pred. No. 4.2; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rishinoto, Tadamitsu
APPLICANT: Hirano, Toshio
APPLICANT: Akira, Shizuo
APPLICANT: Tanabe, Osamu
APPLICANT: Tanabe, Osamu
APPLICANT: Kinoshita, Shigami
APPLICANT: Kinoshita, Shigami
APPLICANT: Shimamoto, Takuya
TITLE OF INVENTION: C/EBP2 Gene and Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POSYMS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/601,094
FILING DATE: 19901022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION TELECOMMUNICATION: 435
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 293-7060
TELEX: 6491103
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARATERISTICS:
LENGTH: 1914 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/07601094
Patent No. 5215892
                                                                                                                                                                                                                                                                                                     CCATION: 1424

MAME/KEY: UNDRAMION: UNKNOWN

MAME/KEY: UNBUFE

CCATION: 1458

MAME/KEY: CDS

LCCATION: (299)...(1336)

US-09-593-711A-3
                                                                                                                                                                                                                  Query Match 6.8%
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 281..1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COTHER INFORMATION US-07-601-094-1
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US-07-601-094-1
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OTHER INFORMATION: unknown
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LIBRARY: plasn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
LENGTH: 1910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-593-711A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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US-09-018-584A-4
Sequence 4, Application US/09018584A
Sequence 4, Application US/09018584A
Sequence 4, Application US/09018584A
SPELICANT Schumm, James W.
APPLICANT: Schumm, James W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
TITLE OF INVENTION: REPEAT DNA MARKERS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
US-08-594-031-84/C
Sequence 84, Application US/08594031
Sequence 84, Application US/08594031
Sequence 84, Application US/08594031
SERRAL INFORMATION:
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESSE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.8%; Score 18; DB 1; Length 252; Best Local Similarity 100.0%; Pred. No. 4.6; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36,902
ER: 0A146-0110
                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS SOFTWARE: FASTEM: DOS SOFTWARE: FASTEM: DOS SOFTWARE: FASTEM: DOS SOFTWARE: PASTEM: DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2800 Woods Hollow Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 84: SEQUENCE CHARACTERISTICS: LENGTH: 252 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO

ANTI SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:
US-08-594-031-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Madison
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                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.8%; Score 18; DB 4; Length 317;
100.0%; Pred. No. 4.6;
tive 0; Mismatches 0; Indels
COUNTRY: U.S.A.
ZIP: 53711-5399
COMPUTER READBLE FORM:
MEDLUM TYPE: Diskette - 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible PC
COMPUTER: IBM Compatible PC
COMPUTER: IBM COMPATIBLE ACT
COMPUTER: US OF OWNING STEAM
SOFTWARE: WORD 97 (DOS text format)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,584A
FILING DATE: 04-Feb-1998
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Grady J. Frenchick
REGISTRATION NUMBER: 29,018
REFERENCE/DOCKET NUMBER: 16026.9180
TELEPHONE: (608) 257-3591
TELEPHONE: (608) 257-3551
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3. Application US/09593711A
Patent No. 6271030
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Madeline M. Butler
APPLICANT: Jacqueline Wyatt
TILE OF INVENTON:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/593,711A
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7: plasmid, pGem3Zf(+)
C331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Circular
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 atgttttgttttgtttg 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 ATGTTTGTTTTGTTTTG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
NAME/KEY: unsure
LOCATION: 1415
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 1421
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NAME/KEY: unsure
LOCATION: 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.8
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 317 bp
TYPE: Nucleic Acid
STRANDEDNESS: Double
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Sequence 35, Appl Sequence 35, Appl Sequence 169, Appl Sequence 169, Appl Sequence 119, Appl Sequence 15, Appl Sequence 12, Appl Sequence 13, Appl

US-08-642-274D-35 US-08-952-014C-35 US-08-991-784A-169 US-08-091-784A-169 US-09-062-451-169 PCT-US96-10521-19 PCT-US96-10521-15 US-08-618-408B-3 US-08-618-408B-3 US-08-618-408B-3 US-08-618-408B-3 US-08-618-408B-3 US-08-618-3 US-08-909-965C-13 US-08-480-784-13 US-08-483-553-13 US-08-483-554B-13 US-08-483-554B-13 US-08-483-554B-13 US-08-483-554B-13

228 330 331 331 444 445 444 445 445 445 445

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; Search time 139.75 Seconds
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465.781 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                               383533 seqs, 122816752 residues
                                                                                                     September 20, 2002, 09:51:18
                                                                    OM nucleic - nucleic search, using sw model
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Post-processing: Listing first 45 summaries

seq length: 0 seq length: 200000000

Minimum DB Maximum DB Database : Issued_patents_NA:*
1: \cgn2_6\ptodata/2\ina/5A_COMB.seq:*
1: \cgn2_6\ptodata/2\ina/5B_COMB.seq:*
3: \cgn2_6\ptodata/2\ina/6A_COMB.seq:*
4: \cgn2_6\ptodata/2\ina/6A_COMB.seq:*
5: \cgn2_6\ptodata/2\ina/6B_COMB.seq:*
6: \cgn2_6\ptodata/2\ina/PCTUS_COMB.seq:*
6: \cgn2_6\ptodata/2\ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 51, Appl	84,	4, 4	6	H	7	4	Sequence 1, Appli	7	Sequence 2, Appli	20	21,	22,	83,	2, 4	3, 1	99	3, 1	'n	Sequence 6, Appli	Sequence 29, Appl	29,	27,	28,	Sequence 1, Appli	Sequence 10, Appl	37,
SOMMAKES		ΔI	US-09-247-155-51	US-08-594-031-84	US-09-018-584A-4	US-09-593-711A-3	US-07-601-094-1	US-08-012-735-1	US-09-117-927-4	US-08-909-965C-1	US-08-162-146-2	US-09-314-127-2	US-08-724-394A-20	US-08-724-394A-21	US-08-724-394A-22	US-09-106-038A-83	US-09-407-675-2	US-08-637-115-3	US-09-276-531-66	US-09-018-584A-3	US-09-018-584A-2	US-09-018-584A-6	US-08-686-878A-29	US-09-175-928-29	PCT-US92-01691-27	PCT-US92-01691-28	US-08-221-767-1	US-09-342-681C-10	US-09-018-584A-37
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Indels

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Mismatches

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Matches

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US-09-247-155-51/c Sequence 51, Application US/09247155A	
Patent No. 6312922 GENERAL INFORMATION:	
APPLICANT: Dumas Milne Edwards, Jean-Baptiste	
APPLICANT: Duclert, Aymeric	
AFFLICANI: BOUGUELELEC, LYGIE TITLE OF INVENTION: Complementary DNAS	
FILE REFERENCE: GENSET.021A	
EARLIER APPLICATION NUMBER: 60/0/4,121	
EARLIER APPLICATION NUMBER: 60/099,273	
EARLIER FILING DATE: 1998-10-04	
SEQ ID NO 51	
LENGTH: 687	
TYPE: DNA	
ORGANISM: Homo sapiens	
LOCATION: 67222	
NAME/KEI: SIG_PEPTIGE	
LOCATION: 6/159	
OTHER INFORMATION: SCORE 5.8	
NAME /KEV: DOLVE gite	
TOCATION 673 687	
-09-247-155-51	

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qq Search completed: September 20, 2002, 10:00:07 Job time: 11725 sec

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9705-0047612
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970S-0047501.
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970S-0047581.
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97us-0056632.
97us-0056636.
                             98WO-US04493
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     W09839448-A2
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11-APR-1997;
11-APR-1997;
11-APR-1997;
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22-AUG-1997;
22-AUG-1997;
                 11-SEP-1998
                             06-MAR-1998,
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Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA, Freng P, Ferrite AM, Fischer CL, Florence RA, Greene JM, Hu JS, Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA; Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human genes and the secreted polypeptide(s) they encon- useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 293-294; 721pp; English.
                                                                                                                                                      9703-0056875.
9703-0056875.
9703-0056876.
9703-0056877.
9703-0056878.
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97US-0056884.
97US-0056886.
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970S-0056910-
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97US-0056903.
97US-0056908.
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97US-0056892
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P-PSDB; AAW74792.
                                                                                                                                                                                                                                                                                                                                           22 - AUG - 1997;
23 - AUG - 1997;
25 - AUG - 1997;
26 - AUG - 1997;
27 - AUG - 1997;
28 - AUG - 1997;
20 - A
22-AUG-1997,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-1997;
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This sequence represents a nucleic acid molecule designated Gene 62 from the human cDMA clone HATDT67 (deposited as clone ATCC 97900 and ATCC 909046) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAV59502) for increasing the stability of the invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74711-W75026) which are useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for described uses).

Sequence 713 BP; 252 A; 115 C; 98 G; 248 T; 0 other;

ö Query Match 7.2%; Score 19; DB 19; Length 713; Best Local Similarity 100.0%; Pred. No. 9.9; Matches 19; Conservative 0; Mismatches 0; Indels

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P-PSDB; AAY59665
                                                                                                                                               (GEST ) GENSET
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                                          09-FEB-1999;
                                                                       09-FEB-1998
                                                                                    13-APR-1998;
10-AUG-1998;
                                                                                                                 04-SEP-1998
            12-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV59572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with blaulphite, of genes associated with tumour suppression and concogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences.

CS and sequences complementary to (Ss). The nucleic acid may be a complementer (PNA) of at least 9 nucleotides and may be compared in single nucleide polymorphisms and also to be used in an carray for analysing diseases associated with CPG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for a secritarining genetic and/or pepigenetic parameters for the diagnosis.

CC ascertaining genetic and/or pepigenetic parameters may be compared to another set of genetic and/or epigenetic parameters may be compared to another set of genetic and/or epigenetic parameters which are disadvantageous to patients. The present sequence is one of the differences serving as basis for diagnosis and/or pergenetic parameters which are disadvantageous to patients. The present sequence is one of the concogenes. Sequences derived from tumour suppressor genes and concogenes. Sequences derived from tumour suppressor genes and concogenes. Sequences with even numbered Seq ID numbers are the compared complementary sequence of the corresponding odd numbered sequence (e.g. complementary sequence of the corresponding odd numbered sequence (e.g. c.g. is missien).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                              Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy; autoimmune disease; rheumatic disease; embryogenic disorder; myopathy; renal injury; amino aciduria; hypoglycaemia; male rat infertility; hypertension; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein; fingerprint identification technique; chromosome mapping; human; hereditary disease; diagnosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5%; Score 20; DB 22; Length 38342; 00.0%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38342 BP; 12471 A; 472 C; 7153 G; 18246 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein EST coding sequence 108-004-5-0-F5-FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.9
Mismatches
                                                                                                                                                                            Claim 1; SEQ ID No 470; 27pp; English.
                                          Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
                                          Piepenbrock C,
            (EPIG-) EPIGENOMICS AG
                                                                       WPI; 2001-602752/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9940189-A2.
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                                          olek A,
                                                                                                                                                cancer
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contracted cubbas (or genomic DNAs obtainable from them) may be used to prepare PCR primers and probes. These are useful for forensic matching or prepare PCR primers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in alternative fingerprint identification techniques. Antibodies against the proteins encoded by the extended cobhs are useful in identification of proteins encoded by the extended cobhs are useful in identification of tissue types or cell species, as well as identifying tissue specific colluble proteins. The sequences can be used for chromosome mapping and identification of genes associated with hereditary diseases or drug response. Signal sequences from the cDNAs can be used in construction of secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstream genomic DNA sequences including promoters. This is in turn useful for identifying proteins that interact with promoter sequences. Some of the proteins may be useful in diagnosting and treating several disorders including, but not limited to: cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders, audimune diseases, and rheumatic diseases, embryogenic disorders, hypertension, renal injury, anino acidurias, hypoglycaemia, male rat infertility and myopathies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Extended cDNAs useful for expressing secreted proteins and to obtain specific antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes a human secreted protein of the invention.
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100.0%; Pred. No. 9.9;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Bougueleret L, Duclert A, Dumas Milne Edwards J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein gene 62 clone HATDT67.
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99WO-IB00282
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Best Local Similarity 100.
Matches 19; Conservative
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2000US-0249297

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2000US-0232399.
2000US-0232400.
2000US-0232401.
2000US-0233063.
2000US-0233064.
2000US-0233065.
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2-OCT-2000;
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08-NOV-2000;
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L-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
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                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 7364; 1297pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                       Rosen CA, Barash SC, Ruben SM;
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17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0250160.
01-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251088.
06-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
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2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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Best Local Similarity
Matches 20; Conserv
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06-APR-2000;
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                                                      RESULT 12
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2000US-0246528
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08 - NOV - 2000;
17 - NOV - 2000;
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11-DEC-2000)
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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                    Human reproductive system related antigen DNA SEQ ID NO: 7364.
AAL04676 standard; DNA; 32249 BP
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20000S-0220964.
20000S-0224518.
20000S-0224519.
20000S-0225213.
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2000US-0190076
2000US-0198123.
2000US-0205515.
2000US-0214886.
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2000US-0216847.
2000US-0216847.
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2000US-0225268.
2000US-0225270.
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2000US-0218290.
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                       (first entry)
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Gaps

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7.5%; Score 20; DB 22; Length 5862; 100.0%; Pred. No. 3.1; ive 0; Mismatches 0; Indels

Conservative

Best Local Similarity Matches 20; Conserv

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2000US-0225214
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14 - AUG - 2000;
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                                                                       The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of coldoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. ADS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. themosphilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. influenza). The polypucleotides of the invention can also be used in gene therapy.

AAS1085-AAS42192 represent DNA sequences encoding for the novel human caryme polypeptides of the invention.
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                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
\begin{tabular}{ll} \textbf{pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases} & - \end{tabular}
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                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                Disclosure; SEQ ID No 2097; 1180pp; English.
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Mismatches
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2000US-0190076
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24 - FEB - 2000;

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27 - FEB - 2000;

16 - MAR - 2000;

17 - MAR - 2000;

19 - MAY - 2000;

19 - MAY - 2000;

20 - JUN - 2000;

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70 - JUL - 2000;

11 - JUL - 2000;
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26-JUL-2000;
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16-AUG-2000;
16-AUG-2000;
16-AUG-2000;
16-SEP-2000;
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20000S-0249300 2000US-0249300 2000US-0250160 2000US-0251988 2000US-025198 2000US-0251479 2000US-0251856 2000US-0251868 2000US-0251868 2000US-0237037. 2000US-0237038. 2000US-0237039. 2000US-0237040. 2000US-0239935. 2000US-0240960. 20000S - 0241786 20000S - 0241809 20000S - 0241809 20000S - 0246475 20000S - 0246475 20000S - 0246475 20000S - 0246476 20000S - 0246476 20000S - 0246476 20000S - 0246476 20000S - 0246525 20000S - 0246526 20000S - 0246610 20000S - 0246610 20000S - 0246610 20000S - 0246610 20000S - 0246526 20000S - 0246526 20000S - 0246527 20000S - 0249207 20000S - 0249216 20000S - 0249216 20000S - 0249217 2000US-0241221. 2000US-0241785 02.0CT-2000; 20.0CT-2000; 20.0C 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2

SM Ruben HUMA-) HUMAN GENOME SCI INC Rosen CA, Barash SC,

WPI; 2001-465566/50

Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive,

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2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251869.
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17-NOV-2000;
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The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU3814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. athritis), neurological disorders (e.g. athritis), neurological disorders (e.g. athreosclerosis), blood-related disorders (e.g. athreosclerosis), c.g. infertility) and infectious disorders (e.g. athreosclerosis), blood-related disorders (e.g. the invention can also be used in gene therapy. AAS41685-AAS4192 represent DNA sequences encoding for the novel human enzyme polypeptides of the invention can also be used in gene therapy. AAS41685-AAS42192 represent DNA sequences encoding for the novel human enzyme polypeptides of the invention. Can also be used in gene therapy. AAS41685-AAS42192 represent DNA sequences encoding for the novel human enzyme polypeptides of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO at ftp. wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                             Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
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                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID No 2096; 1180pp; English.
                                                                                                                                      Rosen CA, Barash SC, Ruben SM;
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Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
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                                          05-JAN-2001; 2001US-0259678.
08-DEC-2000; 2000US-0251990
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autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ds.
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2000US-0205515
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06-SEP-2000;
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30-JUN-2000;
07-JUL-2000;
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14-AUG-2000;
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22-AUG-2000;
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01-SEP-2000;
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26-JUL-2000;
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                                                                                       Human; foetal protein; cytostatic; immunosuppressive; immunostimulant; nootropic, neuroprotective; thrombolytic; osteopathic; antiinflammatory; gene therapy; antisense therapy; cancer; immune disorder; growth disorder; osteoporosis; thrombolytic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel fetal proteins useful for the treatment and diagnosis of diseases associated with dysfunction of the protein e.g. cancers, immune disorders, growth disorders, thrombolytic disorders, nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder;
                                                                                                                                                  nervous system disorder; inflammation; expressed sequence tag; EST; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel foetal polypeptides encoded by polynuclectides comprising one of 477 sequences fully defined in the specification. The foetal polynuclectides and polypeptides are useful in the treatment and diagnosis of diseases such as cancers, immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, nervous system disorders and inflammation. The present sequence is a full length cDNA which was assembled using expressed sequence tags (ESTs) found to be expressed in human foetal tissue
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Pred. No.
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Zhou P, Werhman T;
                                                         Human foetal cDNA, SEQ ID NO: 1231
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100.0%; Pre
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15-SEP-2000; 2000US-0663870.
06-NOV-2000; 2000US-0707351.
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Liu C, Yeung

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Length 619 DB 21; Pred. No. 3. Score 20; 100.08; F1 264 9905 - 0151065 9905 - 0151066 9905 - 0151308 9905 - 0151308 9905 - 0151307 9905 - 0151307 9905 - 0153758 9905 - 0153778 9905 - 0154018 9905 - 0154018 9905 - 0155486 9905 - 0155486 9905 - 0155486 9905 - 0155486 9905 - 0155486 9905 - 0155486 9905 - 0155486 9905 - 0155486 9905 - 0158329 9905 - 0158329 9905 - 0158329 9905 - 0158329 9905 - 0158329 9905 - 0159330 9905 - 0159330 9905 - 0159330 9905 - 0159330 9905 - 0159330 9905 - 0159330 9905 - 0159330 9905 - 0159330 9905 - 0159330 9905 - 0159330 9905 - 0159330 9905 - 0159330 9905 - 0159330 9905 - 0159330 9905 - 0159330 99US-0149723. 99US-0149723. 99US-0149929. 99US-0149902. 99US-0149930. 99US-0150566. 99US-0150884. 990S-0161359. 990S-0161360. 990S-0161361. 990S-0161920. 99US-0161992. 99US-0161993. 99US-0162142. 99US-0161405. 99US-0160981 99US-0160989 99US-0161404 Query Match 7.5 Best Local Similarity 100. Matches 20; Conservative 18-AUG-1999,
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Gaps

BP.

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pp

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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Gaps

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us-09-802-520-9.rng

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misc_feature

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               Gaps
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0
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Ouery Match

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The present invention relates to Mc1-1 gene regulatory elements and the variant Mc1-1s/deltaTM. The anti-apoptotic Mc1-1 protein is encoded by exons 1, 2 and 3 The pro-apoptotic Mc1-1s/DeltaTM variant encoded by exons 1 and 3 is obtained due to alternative mRNA splicing. The Mc1-1 gene regulatory element is useful for modulating the Mc1-1 gene expression in a cell e.g., neuronal cell or tumour cell, such that apoptosis of the cell is induced or cell viability is increased. The Mc1-1 and its regulatory elements are used for treating pathological conditions which include cancer, diabetic retinopathy, corneal graft necvascularisation and neovascular glaucoma, epithelial conditions such as psoriasis, autoimmune diseases like rheumatoid arthritis, systemic lupus erythematosus, and neurodegenerative diseases. The present genomic DNA sequence encodes Mc1-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel Mc1-1 gene regulatory elements, useful for modulating expression of Mc1-1 polypeptide or its variant which regulate apoptosis in neuronal or tumor cells -
                                                                                                                                                      vo adjacent initiator
the transcription start site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8253 BP; 2153 A; 1815 C; 1959 G; 2326 T; 0 other;
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                                           misc_signal
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                                                                                                                                                                                                                                                                                                                                                                               exon
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Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer;

Human;

Human DNA for Six-Transmembrane Protein of Prostate 1, STMP1.

16-JAN-2002 (first entry)

benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorochidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ds.

b "Represents 12713 nucleotides of intron 2"

*tag= a note= "Represents 338 nucleotides of intron 1"

Location/Qualifiers

Homo sapiens

*tag=

misc_feature

misc_feature

d "Represents 1396 nucleotides of introm 3"

/note= 1225 /*tag=

misc_feature

/*tag= 'note=

/*tag=

misc_feature

WO200172962-A2

04-OCT-2001

"STMP1"

/product ...

misc_feature

/note= "Re 200..1702 *tag=

CDS

e "Represents 2372 nucleotides of introm 4"

'note= "Represents 2299 nucleotides of intron 5"

24-MAR-2000; 2000US-191929P. 23-MAR-2001; 2001WO-US09410.

(SAAT/) SAATCIOGLU F.

WPI; 2001-662926/76. P-PSDB; AAU10187

Saatcioglu F;

m

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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence encodes a prostate specific protein, Six-Transmembrane
                                                                    Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                                                  benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptocothidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ss.
                                  Human cDNA encoding Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1680 BP; 467 A; 334 C; 373 G; 506 T; 0 other;
                                                                                                                                                                                                      Location/Qualifiers
178..1650
/*tag= a
                                                                                                                                                                                                                                                         /product- "STMP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 4E; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               24-MAR-2000; 2000US-191929P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prostate 1, STMP1
                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09410.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 (SAAT/) SAATCIOGLU F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-662926/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAU10187
                                                                                                                                                                                                                                                                                         WO200172962-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saatcioglu F;
                                                                                                                                                                        Homo sapiens
16-JAN-2002
                                                                                                                                                                                                                                                                                                                             04-OCT-2001
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testis specific polypeptides and the nucleic acids encoding them.
Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids, antisense molecules for the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatilis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished cryptorchidism, undescended, retractile, ascending or vanished used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The prostation of the protein protein, Six-Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein of Prostate 1, STMP1
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                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                      Length 1680;
                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                               Score 54; DB 22; I
Pred. No. 7.5e-17;
0; Mismatches 0;
                                                                                                                                    20.4%; Scu-
100.0%; Pre
0;
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Conservative

54;

Similarity

Query Match Best Local S

Best Loc Matches

Sequence 1725 BP; 476 A; 340 C; 387 G; 517 T; 5 other;

AAS15793 standard; DNA; 1725 BP

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AAS15793 RESULT

AAS15793;

New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids

The invention relates to substantially pure prostate-specific or

Example 3; Fig 4B; 114pp; English.

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                                                                                                                                                                                                                                                                                                                                                        used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer and lung cancer. The present sequence represents partial exon 6/3' UTR sequence of a prostate specific protein, Six Transsmembrane Protein of Prostate 1, STMP1.
                                                                                                              The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer, penign cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer;
New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ccggagagggtcacagtaatgtgatgataaatggtgttcacagctgccatataaagttct 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 265; DB 22; Length 2381; 100.0%; Pred. No. 5.2e-120; ative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ORF of Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2381 BP; 780 A; 415 C; 387 G; 799 T; 0 other;
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178..1650
/*tag= a
/product= "STMP1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS15801 standard; cDNA; 4329 BP
                                                                            Claim 6; Fig 4C; 114pp; English.
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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them.

Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign of the testis or prostate prostatifis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence represents the open reading frame of a prostate prestific protein, Six-Transmembrane Protein of Prostate 1, STMPI.
                                                                                                                                                                                                                                                                 New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   actcatgccattatttttatgacttctacgttcagttacaagtatgctgtcaaattatcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 265; DB 22;
; Pred. No. 5.1e-120;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Fig 4D; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
100.0%;
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                                                                               23-MAR-2001; 2001WO-US09410
                                                                                                                 24-MAR-2000; 2000US-191929P
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                                                                                                                                                                                                                   WPI; 2001-662926/76.
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Best Local Similarity
Matches 265; Conserv
                                                                                                                                                                                                                                   P-PSDB; AAU10187
              WO200172962-A2.
                                                                                                                                                                                   Saatcioglu F;
                                              04-OCT-2001
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September 20, 2002, 09:59:59; Search time 600.75 Seconds (without alignments) 757.357 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. - nucleic search, using sw model US-09-802-520-9 OM nucleic Run on:

Perfect score: Sequence:

OLIGO_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

1736436 seqs, 858457221 residues Searched:

Total number of hits satisfying chosen parameters: 0 Word size

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length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human Six-Transmem	Human ORF of Six-T	Human cDNA encodin	Human DNA for Six-	Human Mcl-1 genomi	Arabidopsis thalia	Arabidopsis thalia	Human foetal cDNA,	Genomic sequence #
ID	AAS15800	AAS15801	AAS15802	AAS15793	AAD06430	AAC45859	AAC38598	AAH94544	AAS41970
0.8	22	22	22	22	22	21	21	22	22
Query Match Length DB	2381	4329	1680	1725	8253	617	619	1158	3702
Query Match	100.0	100.0	20.4	17.7	7.9	7.5	7.5	7.5	7.5
Score	265	265	54	47	21	20	20	20	20
Result No.	1	7	3	4	S	ر د	c 2	80	6

Genomic sequence # Human reproductive	Human reproductive	Tumour suppressor	Secreted protein E	Human secreted pro	Human secreted pro	Sequence encoding	Human sub-unit C o		Drosophila melanog			Human immune/haema	Human immune syste	Human nervous syst	Human reproductive	Human immune/haema	Human gene signatu	Activated T-cell d	Human gene signatu	Human immune/haema	Murine metastatic	Human secreted pro	Rat differential t	EST clone GE89. H	Human gene express	Human gene express	Human DNA marker c	Human breast cance	Novel human diagno	Human polynucleoti	Human immune/haema	Human immune/haema	Human polynucleoti	Human immune/haema
22 AAS41971 22 AAL04675					9 AAV59732	Α,	2 AAI68377	3 ABL02241		2 AAS30025	-					-		-		·	-			•	-		-	2 AAL13325	2 AAS39218	-	-	_		2 AAK83957
3842 2		38342 2											9963 2	6229	6229									259 2						414 2				455 2
7.5		٦.	.2	۲.	۲.	۲.		•		•		•	•			٠	•	•	٠		•		•	8.9	•	•		•		8.9	•			•
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10	12	13	c 14	15	16	c 17	18	Н	c 20	21	c 22	23	24	25	26	27	28		c 30	31	c 32	33	34	35	36	37	38			c 41			44	c 45

ALIGNMENTS

AAS15800 standard; DNA; 2381 AAS15800; AAS15800

Н

BP.

(first entry) 16-JAN-2002 Human Six-Transmembrane Protein of Prostate 1, STMP1, exon 6/3' UTR.

Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hypersplasia; acute prostatitis; testicular adnoer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ds; exon 6.

Homo sapiens,

WO200172962-A2.

04-0CT-2001.

23-MAR-2001; 2001WO-US09410

24-MAR-2000; 2000US-191929P.

(SAAT/) SAATCIOGLU

Saatcioglu F;

WPI; 2001-662926/76

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                                                                                                                                                                                                                                                                                                           AL645757 140554 bp DNA linear HTG 08-FEB-2002 Mus musculus chromosome 3 clone XXbac-340J1, *** SEQUENCING IN PROCRESS ***, in unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 10, 2002 this sequence version replaced gi:17384176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 139891 bases at least Q40
Consensus quality: 139899 bases at least Q20
Insert size: 140154; sum-of-contigs
Insert size: 14255; 2.7% error; agarose-fp
Quality coverage: 12.79x in Q20 bases; sum-of-contigs Quality
coverage: 12.58x in Q20 bases; agarose-fp
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                            ALGASTST.10 GI:18643801
HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                              Length 135005;
                                                                                                          0; Indels
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1.40212
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46588. 49183
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49284. .130162
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                                                            Ouery Match 7.9%; Score 21; DB 9; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 21; Conservative 0; Mismatches
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match: proteins: Tr:Q9P0F6"
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                                                                                                                                                                                    Db 38364 GGTATGTTTTGTTTTG 38384
                                                                                                                                                    244 ggtatgttttgttttgttttg 264
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KEYWORDS
SOURCE
ORGANISM
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TITLE
                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
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                                                                                                                                                                                                                                                                                 AL645757
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
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405 others
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ORIGIN
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Gaps ö DB 2; Length 140554; 1.8; Indels ő Query Match 7.9%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 1.6 Matches 21; Conservative 0; Mismatches

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244 ggtatgttttgttttgttttg 264

DD 12877 GGRAFGITITGITITGITTTG 12897

Search completed: September 20, 2002, 09:59:39 Job time: 13437 sec

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repeat_region
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21805. .21860,23543. .23616,25170. .25238,64145. .64226,
64997. .65114,62216. .65349,65443. .65569,67296. .67384,
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/poin(8430. 8744,9242. 9378,21173. 21329,21570. 21633, 21860,23543. 23616,25170. 25238,64145. 64226,64997. 65114,65116. 65349,65443. 65569,67296. 67384,667883,67682. 67859,67953. 68141,71223. 71420,
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1810. 1924
// note="Alusx repeat: matches 185. 300 of consensus"
2190. 2272
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2297. 2598
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2910. 3043
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                                                                                                                                            consensus
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                                                                                                                                                854. .1142

// note="AluSx repeat: matches 1. .302

complement(1112. .1474)

// note="match: GSS: Em:B40114"

1446. .1546

// note="WRER69 repeat: matches 2404. .2
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gene

CDS

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GYARSCSSASPRGFAPSPGSQQSGYGGGLGAGLGGYGAPGYNGLGYPGSPSFLNGSTA
TSPRAIMPSSPPLAAASSMSLPAAAPTTSVFSFSPVNMISAVKQRSAFAPVLRPPSSSP
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11786. .12097
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Gaps

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of AL390202 from base 600001 (AL390202 Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, Calbo Lash, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 23, 2000 this sequence version replaced gi:6468345.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 happing Group. Further information can be found at http://www.sanger.ac.uk/HOPC/Mr20

This sequence is the entire insert of clone RPS-860F19 The true right end of clone RPS-1055616 is at 4586 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by testriction digest. RPS-860F19 is from that he library RRCI-5 constructed by the group of Pieter de Jong. For head etails see
                                                                                                                                                                                                                                                                                                                                                                                                                         HS860F19
HS980F19
Human DNA sequence from clone RPS-860F19 on chromosome 20p12.3-13
Contains the gene for K1AA1442 (similar to olfactory neuronal
transcription factors (COE1, COE2, COE3, EBF3, OLF1), RPL19 (60S
ribosomal protein L19) and HSPC080 pseudogenes, the gene for
metallocarboxypeptidase (CPX-1) and a novel gene. Contains ESTS,
STSS, GSSs and four CpG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 135005)
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1.9;
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HTG; COE; CpG island; CPX-1; EBF3; KIAAl442;
metallocarboxypeptidase; OLF1; RPL19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
                                                                                                                                                                                                             Query Match 7.9%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 1.5 Matches 21; Conservative 0; Mismatches
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                        510000
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300001
400001
500001
700001
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                    AL390202_04
AL390202_05
AL390202_06
AL390202_07
AL390202_08
AL390202_09
Continuation (7 of 10) or
    AL390202_03
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VERSION
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JOURNAL
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11043. .12544
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/note="assembly_fragment"
21175. .22647
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22748. .24713
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/note="assembly_fragment"
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'note="assembly_fragment"
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24814. .26482
1. .109395
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-115013"
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3ap of 100 bp 10
44: gap of 100 bp
.3988: contig of 1344 bp in length
                                       p of 100 bp
contig of 1123 bp in length
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38371: contig of 1735 bp in length

71: gap of 100 bp

100 bp

95: gap of 100 bp

42196: contig of 1701 bp in length
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Location/Qualifiers
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29622: contig of 1450 bp in length
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24713: contig of 1966 bp in length
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86154; contig of 4647 bp in length
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                                                                                                                                                                                                                                                                                 ACU13742 109395 bp DNA linear HTG 20-SEP-2000 Homo sapiens clone RP11-115013, *** SEQUENCING IN PROGRESS ***, 46 unordered pieces.
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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of 1192 bp in length
100 bp
of 1030 bp in length
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of 1083 bp in length
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of 1056 bp in length
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                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-115013
Unpublished
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5957: c
6057: gap c
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                                                                                               VERSION
KEYWORDS
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ORGANISM
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                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
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JOURNAL
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AC013742
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COMMENT

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Where differences are found these are annotated as variations
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ORIGIN
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AL592167 6 GI:15147697
HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRAAPLEEMEAPAADAIMSPEEELDGYEPEPLGKRPAVLPLLELVGESGNNTSTDGSL
PSTPPPAEEEEDDLYRQSLEIISRYLREQATGAKDTKPMGRSGATSRKALETLRRVGD
GVRNHEFTAFGGWVCGVLPCRGPRRWHQECAAGFCRCCWSRSWFGISNKIALL"
join(1727. 2414,2766. 3013,3768. 3884)
/gene="MCL-1"
/note="anti-apoptotic Bc1-2 family member"
                                                                                                                                                                                                                                                                                                                                                                     /product="Mal-1 delta S/TM"
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/protein_id="AaR64256.1"
/brotein_id="7382272"
/translation="WEGLRNAWJGLNLYCGGAGLGAGSGGATRPGGRLLATEKEASA RREIGGGEAGAVIGGSAGASPPSTLTPDSRRVARPPPIGAEVPDYTATPARLLEFAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /procedi_id="AAP64255.1"
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/db_xref="G1:7582271"
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RRAAPLEEMEAPAADAIMSPEEELDGYEPEPLGKRPAVLPLLELVGESGNNTSTDGSL
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HLKTINQESCIEPLAESITDVLVRTKRDWLVKQRGWDGFVEFFHVEDLEGGIRNVLLA
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                                             /note="isolated from a human leukocyte genomic library in EMBL-3 from Clonetech (HL 10006d)" join(1657. .2414,3768. .6703) /gene="MCL-1"
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On Aug 10, 2001 this sequence version replaced gi:14626209.
During sequence assembly data is compared from overlapping clones.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10917)
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                                                                                                                                                                                                                                                                                                              /hote="alternatively spliced isoform of Mcl-1 has a pro-apoptotic function."
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Pred. No. 2.4;
                                                                                                                                                            join(1657. .2414,2766. .3013,3768. .6703)
/gene="MCL-1"
/product="Mcl-1"
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/gene="MCL-1"
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                                                                                                                                               /product="Mcl-1 delta S/TM"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="leukocyte"
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                                                                                                                                                                                                                                1657. .6703
/gene="MCL-1"
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Direct Submission
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AL592167/C
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together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone: and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP attabase can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Purther information can be found at
http://www.sanger.ac.uk/HGP/Chr13
RPI1.14H2 is from the library RPCI-11.1 constructed by the group of http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VECTOR: pBACe3.6

The program of the entire insert of clone inportant. This sequence is not the entire insert of clone RP11-14H2 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP11-181D10 is at 8918 in this sequence. In the true right end of clone RP11-89L15 is at 2000 in this sequence. Location/Qualifiers
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Anote-"L2 repeat: matches 2020. .2314 of consensus"
A217. 4276
Anote-"2 copies 30 mer 91% conserved"
Anote-"Alusx repeat: matches 1. .312 of consensus"
10450. 10585
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.7note-"61 copies 2 mer aa 61% conserved"

2931. .3016

/note="MIR repeat: matches 151. .233 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2301. .2424 /
/note="MER5A repeat: matches 3. .125 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 47. .161 of consensus"
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/note="LlMD2 repeat: matches 5872. .5928 of
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10793. .10894
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/db_xref="taxon:9606"
/chromosome="13"
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Pred. No.
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80. .177
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Best Local Similarity 100.0%; Pr
Matches 21; Conservative 0;
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107455 107544: contig of 100 bp 100 bp 118282: contig of 10738 bp in length 118283 118382: contig of 10738 bp in length 118283 118382: contig of 100 bp 118383 130386: contig of 12004 bp in length 130387 130486: gap of 100 bp 142984 143083: contig of 12497 bp in length 143084 159402: contig of 16319 bp in length 159502: gap of 100 bp 159502: gap of 100 bp 159502: gap of 100 bp 159503 179408: contig of 19906 bp in length.
                                                                                                                                                                                                                                                                                                48938 48937: gap of 100 bp 48938 48937: gap of 100 bp 54468: gap of 100 bp 54468: gap of 100 bp 5469 61661: contig of 7193 bp in length 61662 61761: gap of 100 bp 7235: gap of 100 bp 7235: gap of 100 bp 81163 1262: gap of 100 bp 81163 1262: gap of 100 bp 81163 81262: gap of 100 bp 81263 99914: contig of 7932 bp in length 81959 99216: contig of 9932 bp in length
                                                                                   26424 26523: gap of 100 bp 26524 29526: contig of 3103 bp in length 29627 29726: a 100 bp 29727 34097: contig of 4371 bp in length 34098 34197: gap of 100 bp 37384 37933: contig of 3636 bp in length 3784 37933: gap of 100 bp 37934 43795: contig of 5862 bp in length 37934 43795: contig of 5862 bp in length
100 bp
<sup>r</sup> 3941 bp in length
                          23097: contig of 3941 bp in length 97: gap of 100 bp 26423: contig of 3226 bp in length
                                                                                                                                                                                                                                                           43895: gap of 100 bp 48837: contig of 4942 bp in length
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99317 107444: contig of 8128 bp in length
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1. .1105
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'note="assembly_fragment"
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/note="assembly_fragment"
23198. .26423
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'note="assembly_fragment"
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'note="assembly_fragment"
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/note="assembly_fragment"
15244. .19056
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9157. .23097
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26524. .29626
/note="assembly_fragment"
29727. .34097
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'note="assembly_fragment
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/db_xref="taxon:9606"
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/map="8"
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vector_side:right"
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19157 23097: conti-
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26423: conti-
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Craig, R.W., Zhou, P. and Bingle, C.D.
Direct Submission
Submitted (26-02T-1999) Molecular and Genetic Medicine, University
of Sheffield Medical School, Glossop Rd, Sheffield, S Yorks S10
2RX, UK
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 8253)
Bingle,C.D., Craig,R.W., Swales,B.M., Singleton,V., Zhou,P. and
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Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 22; Conservative 0; Mismatches
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36085 c 36807 g 51028 t
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159503. .179408
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1. .8253
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AF198614.1 GI:7582270
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 179408)
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                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                   NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.3%; Score 22; DB 2; Length 171483;
100.0%; Pred. No. 0.53;
iive 0; Mismatches 0; Indels 0
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1325 1424: gap of 100 bp
1425 2513: contig of 1089 bp in length
2514 23113: contig of 20500 bp in length
23114 23213: gap of 100 bp
23114 23213: gap of 100 bp
23214 51238: contig of 28025 bp in length
                                                                                                                                                                                                                                                                                                                 51239 51338: gap of 5 100 bp 51339 51339 81239: contig of 29901 bp in length 81240 81339: gap of 100 bp 81340 17483: contig of 90144 bp in length. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 170983; sum-of-contigs
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33837 c 35795 g 52521 t
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23214. .51238
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51339. .81239
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HTG: HTGS_PHASE1; HTGS_DRAFT.
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81340. .171483
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Badderion, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Grand, J.C., Illev, M., Grand, G., Grand-Pierre, N., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Kand, J., Kan, L., L., Kan, L., L., Kan, L., L., Lauccque, K., Johnson, R., Johnson, R., Johnson, R., McCarthy, M., McCarthy, M., McCarthy, M., McCarthy, M., McCarthy, M., McCarthy, P., McGurk, K., McMerers, T., Lehoczky, J., McTond, T., Mranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T., M., Ollver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stanger, Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vong, G., Zainoun, J., Zimmer, A. and Zody, M., Tigillo, M., Tirgillo, M., Tirgillo, M., Tirgillo, M., Vong, G., Zainoun, J., Zimmer, A. and Zody, M., Tepeats were identified using Repeatmasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/Repeatmasker:
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Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 165594 bases at least Q40
Consensus quality: 172613 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 185000; agarose-fp
Insert size: 176708; sum-of-contigs
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Quality coverage: 4.1 in Q20 bases; sum-of-contigs
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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:: gap of 100 bp
2470: contig of 1265 bp in length
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contig of 3813 bp in length
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4687: con
4787: gap of
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3411. .34142
/note="MIR repeat: matches 117. .148 of consensus"
/note="MIR repeat: matches 6207. .7977 of consensus"
/note="LiM04 repeat: matches 6207. .7977 of consensus"
/note="MIR repeat: matches 120. .180 of consensus"
/note="MIR repeat: matches 48. .148 of consensus"
/note="MIR repeat: matches 2570. .2695 of consensus"
/note="L2 repeat: matches 2570. .2695 of consensus"
/note="L2 repeat: matches 2570. .2695 of consensus"
/note="L2 repeat: matches 2575. .2706 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MLTL2" repeat: matches 11. .374 of consensus"
27408. .27641
/note="MIR repeat: matches 15. .261 of consensus"
28885. .29011
/note="MER5A repeat: matches 1. .189 of consensus"
31232. .31277
/note="L2 repeat: matches 2661. .2705 of consensus"
31619. .31685
/note="L2 repeat: matches 2356. .2424 of consensus"
31926. .32125
/note="MIR repeat: matches 57. .254 of consensus"
33172. .33364
/note="MIR repeat: matches 64. .259 of consensus"
33414. .33824
                                                                                                                                                                                                                                                                 1653. 21720

Indem"MIR repeat: matches 76. .144 of consensus 2001. .2256

2001. .2256

/note="MIR repeat: matches 20. .144 of consensus" 2280. .22463

/note="MIR repeat: matches 35. .122 of consensus" 2884. .24153

/note="MIR repeat: matches 1. .308 of consensus" 2884. .2588

/note="Mir repeat: matches 1. .308 of consensus" 2588

/note="Mir repeat: matches 3686. .3939 of consensus" 25593. .25956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="L1MB5 repeat: matches 5740. .6174 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41096. 41180
/note="MER5B repeat: matches 62. 160 of consensus"
41181. 41349
/note="FRAM repeat: matches 1. 166 of consensus"
                                                                                                /note="L2 repeat: matches 2650. .2706 of consensus"
19668. .20448
                                                                                                               79668. 20448

/note="12 repeat: matches 1944. .2708 of consensus"

2004. .20794

/note="14.0x repeat: matches 23. .312 of consensus"

20795. .20966
'note="MER2 repeat: matches 283. .345 of consensus"
                                                                                                                                                                                                                                                    .2466 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Alujo repeat: matches 1. .301 of consensus"
26369. .26677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MSTA repeat: matches 1. .426 of consensus" 43071. .43269
/note="MIR repeat: matches 47. .256 of consensus" 43631. .44125
/note="LTR33 repeat: matches 6. .509 of consensus" 44270. .44579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MLTlAl repeat: matches 2, .58 of consensus"
41818. .41904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 70. .241 of consensus"
41603. .41661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluY repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .62 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .87 of consensus"
                                                 .202 of consensus"
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/note="MER5B repeat: matches 3.
41446, .41601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSx repeat: matches 1.
26937. .27286
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                                                                                                                                                                                                                                         note="L2 repeat: matches 2272.
                                            /note="MIR repeat: matches 3.
19450. .19503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .41661
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2 (Bases I to 171483)

Bairen, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Carny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.; Donelan, L., Doyle, M., Fertexira, P., FitzHugh, W., Forrest, C., Enke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Maratas, A., Lehoczky, J., Lieu, C., Looke, K., Macdonald, P., Maratas, A., Lehoczky, J., Lieu, C., Looke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Maylor, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavilin, B., Peterson, K., Pollara V., Riley, R., Roberts, D., Roy, A., Severy, P., Stanger Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.

Lire, Lubmitted (12-40G-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on May 25, 2000 this sequence version replaced gi:7248943.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC009278 171483 bp DNA linear HTG 04-MAY-2001
Homo sapiens clone RPl1-44J4, WORKING DRAFT SEQUENCE, 6 unordered
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hömo.
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                                                          .243 of consensus"
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                    /note="Sequence from Clone PCR only. Sequence
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                                                                                                                                                                                                                            Length 64855;
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/note="MIR repeat: matches 2, .243 of con:
45096. .45117
/note="11 copies 2 mer tt 100% conserved"
46347. .46371
                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                            8.3%; Score 22; DB 9;
100.0%; Pred. No. 0.58;
Live 0; Mismatches
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Center clone name: 44_J_4
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AC009278.4 GI:8072422
HTG; HTGS_PHASE1; HTGS_DRAFT.
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Best Local Similarity 100.(
Matches 22; Conservative
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AC009278/c
LOCUS
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TITLE
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AUTHORS
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JOURNAL
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KEYWORDS
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sequence. The true right end of clone RP4-691N7 is at 100 in this
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                                                                     FEATURES
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw., SWISSPROT; Tr:, TREMBL; Wp., WORMPEP; Information on the WORMPEP
                                                                                                                                                                                     EIILSNTKVLEIPLLPENNMRAIIDČAGILKLRNSDIELRKGETDIGRKNTRVRLVFR
VHIPOPNGRTLSLQYASNPIECSORSAQELPLVEKOSTDSYPVIGGKKWVLSGHNFLQ
DSKVIFVERAPDGHHVWEMEAKTDRDLCKPNSLVVEIPPFRNORITSPAQVSFYVCNG
KRKESQYORFTYLPANGNSVELTLLSSESELRGGFY"
1009 c 828 g 823 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMPORTANT: This sequence is not the entire insert of clone RP5-1117P19 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP5-1117P19 is at 64855 in this sequence. The true left end of clone RP6-102010 is at 15181 in this
                                                                                            IKSRKTALEHAPSVALKVEPAGEDLGTTPPTSDFPPEBYTFQHLRKGAFCEQYLSVPQ
ASYQWAKPKSLSPTSYMSPSLPALDWQLPSHSGPYELR1EVQPKSHHRAHYETEGSRG
AVKASAGGHPIVQLHGYLENEPLTLQLFIGTADDRLLRPHAFYQVHRITGKTVSTTSH
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      LPSLEAYRDPSCLSPASSLSSRSCNSEASSYESNYSYPYASPQTSPWQSPCVSPKTTD
                                 PEEGFPRSLGACHLLGSPRHSPSTSPRASITEESWLGARGSRPTSPCNKRKYSLNGRQ
PSCSPHHSPTPSPHGSPRVSVTEDTWLGNTTQYTSSAIVAAINALTTDSTLDLGDGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 11-APR-2001
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RP5-1117P19 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see http://www.chcii.org/bacpac/home.htm
VECTOR: pCYPAC2
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human DNA sequence from clone RP5-1117P19 on chromosome AL139219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3%; Score 22;
100.0%; Pred. No.
ative 0; Mismatch
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Tromans, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity
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/note="L1M3 repeat: matches 5645. .5774 of consensus"
18229. .18289
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12925. .13085
note="MIR repeat: matches 64. .260 of consensus"
13167. .13464
                                                                                                                                                                                                                                                                                             1704. 2002
/note="Alusx repeat: matches 1. .295 of consensus"
2003. 2100
/note="MIR repeat: matches 155. .247 of consensus"
2194. .2525
2789. .3020
                                                                                                                                                                                                                                                                                                                                                                                                                           2789 .3020
/note="L2 repeat: matches 2511. .2745 of consensus"
3106. .3228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3508. .3572
/note="MIR repeat: matches 158. .219 of consensus"
4870. .5108
/note="L2 repeat: matches 2248. .2500 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116. .279
note="L2 repeat: matches 2647. .2709 of consensus"
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                                                                                                                                                                                  'note="L2 repeat: matches 2592. .2698 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2670 of consensus'
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7437. .17554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5551. .5981 /
/note="MLTIC repeat: matches 1. .504 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSx repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .241 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9051. .9170
//note="MIR repeat: matches 47. .173 of consensus"
//note="L2 repeat: matches 2630 .2750 of consensus 9362. .9413
//note="L2 repeat: matches 2648 .2700 of consensus 10063 .10336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .249 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /hote="MIR repeat: matches 66. .239 of consensus"
11287. .11381
//note="MIR repeat: matches 151. .249 of consensus"
11816. .12075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .191 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .149 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6709. .16895
'note="MIR repeat: matches 1. .201 of consensus"
.7155. .17342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7636. 7893
/note="LTR33 repeat: matches 17. .284 of 9051. .9170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2695 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2741 of
                                                                                                                                                                                                                                                           .153 of
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/note="L2 repeat: matches 2696.
15781. 15903
                                                                                                                                                                                                                     779. 872

//note="MIR repeat: matches 46.

1616. 1703

/note="MIR repeat: matches 66.

1704. 2002
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11068. .11234
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'note="MIR repeat: matches 71.
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17977. .18054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat: matches
                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="RP5-1117P19"
               Location/Qualifiers
                                                                                                                                            /clone_lib="RPCI-5"
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10865. .10
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/cell_type="mast"
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100.08; Pr.
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                      /gene="Nfatcb"
9. .2120
                                                        /gene="Nfatcb"
                                                                                /codon_start=1
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    1. .3435
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/product="nuclear factor of activated T cells c"
/protein_id="AAF40255.1"
/db_xref="GI-7208618"
/db_xref="GI-7208618"
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FLSSGNTRRNGAPTLESPRIETTSYLGLHHGSGOFFHDVENSULPSGKRSPSTATH
LFSLEAYRDPGCLEPARSISPSTSREASTESPSYENYSYPASPQTSPWGSPTSTATH
LFSLEAARDFACACHLLGSPRHESPTSPRASITEESWKLGARGSRPTSPCNKRKYSLNGRO
PEGCSPHHSPTPSPHGSPRYSVTEDTWLGNTTQYTSSAIVAAINALTTDSTLDLGDGVP
IKSRKTALBHAPSYALKVERAGEDLGTPPFSDFPFSDFPTFQHLRKGAPCEQYLEVPQ
ASYQWAKRESISPTSYMSPSLPALDWQLPSTGSPSPTRIETSVQPKSHHRAHYETGSSRG
AVKASAGGHPIVQLHGVLENBELLLQLFLLGLFADDRLLRRHARHYETGSTRG
AVKASAGGHPIVQLHGVLENBELLLQLFLLGLFLLGLTLLCAGILKLRNSDIELRKGFTDIGRKNTFVRIFF
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NF-ATC Isoforms are differentially expressed and regulated in murine T and mast cells

L J. Immunol. 155 (5), 2820-2828 (1999).

Sherman, M.A., Powell, D.R., Weiss, D.L. and Brown, M.A.

Direct Submission

Submitted (20-FEB-1998) Experimental Pathology, Emory University, 1639 Pierce Drive, Atlanta, GA 30322, USA

Location/Qualifiers
Submitted (24-FEB-2000) Molecular and Developmental Biology,
Institute of Medical Science, 4-6-1, Shirokanedai, Minato-ku, Tokyo
108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHIDQPNGRTLSLQVASNPIECSQRSAQELPIVEKOSTDSYPVIGGKKMYLSGHNFLQ
DSKVIFVEKAPDGHHVWEMEAKTDRDLCKPNSLVVEIPPFRNGRITSPVQVSFYVCNG
KRKRSQYQRFTYLPANGNSVFLTLSSESELRGGFY"
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Mus musculus transcription factor NF-ATc isoform b (Nfatcb) mRNA,
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ive 0; Mismatches 0; Indels (
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/gene="Nfatc1"
/note="transcription factor"
                                                                                               /organism="Mus musculus"
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/db_xref="taxon:10090"
/cell_line="C15"
/cell_type="mast cell"
                                                                                                               /db_xref="taxon:10090"
/chromosome="18"
                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                  /note="NFATc"
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                                                                                                                                                     /map="18E4"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eu (abases 1 to 3469)
Sherman,M.A., Powell,D.R., Weiss,D.L. and Brown,M.A.
NP-ATC Isoforms are differentially expressed and regulated in murine T and mast cells
I. J. Immunol. 165 (5), 2820-2828 (1999)
S. Chases 1 to 3469)
Sherman,M.A., Powell,D.R., Weiss,D.L. and Brown,M.A.
Direct Submission
I. Sherman,M.A., Powell,D.R., Weiss,D.L. and Brown,M.A.
I. Sherman,M.A., Powell,D.R., Weiss,D.R., Weiss,
                                                                                                                                                                                                                                                                                                                                                                                            PASSLSSRSCNEASSYESNYSYPYASPQTSPWQSPCVSPWTTDPEEGFPRSLGACHL
LGSPRHSPFSTSPRASTTEESWLGARGSRPTSPCNKRKYSLWGRQESCPHISPTPSPH
GSPRYSYTEDTWLGNTTQYTSSAIVABAINALTTDSTLDLGBCVPIKSRKTALEHAPSY
ALKVEPGEDLGTTPPTSDFPPEETTPCPHLKGAFCEQYLSYPQASYQWARRKSLSP
SYMSPSLPALDWQLPSHSGPYELRIEVQPKSHHRAHYETEGSRGAVKASAGGHPIVQL
HGYLEMPRITLTQLFIGTADDRLLRPHAFYQVHRITGKTWYSTSHEILLSNTKYLEIPU
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LESPRIEITSYLGLHHGSGQFFHDVEVEDVLPSCKRSPSTATLHLPSLEAYRDPSCLS
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FLSSGNTRPNGAPTLESPRIEITSYLGLHHGSGQFFHDVEVEDVLPSCKRSPSTATLH
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Mus musculus transcription factor NF-ATC isoform a (NF-ATCa) mRNA,
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/product="transcription factor NF-ATc isoform b" /protein_id="AAC05505.1" /db_xref="G1:2952324"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . _ต
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Pred. No. 0.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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Direct Submission
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ORGANISM
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VERSION
KEYWORDS
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TITLE
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1 (bases 1 to 172915)

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Bletrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Stantipop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC099742
AC099742.1 GI:17017546
HTG; HTGS_PHASE1; HTGS_DRAFT.
olive baboon.
Papio cynocephalus anubis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                         aactgacttagtgatagagttttcttcaagttaattttcacaaatgtcatgtttgccaat 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing Center, 8717
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           AC099742 172915 bp DNA linear HTG 20 Papto cynocephalus anubis clone RP41-167P22, WORKING DRAFT
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0
                                                                                                                                   Length 156214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 171170 bases at least Q40 Consensus quality: 177910 bases at least Q30 Consensus quality: 17236 bases at least Q20
                                                                                                                                                                         Indels
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Center code: NISC
                                                                                                                                 89.4%; Score 237; DB 9; Le
100.0%; Pred. No. 5.2e-114;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (20-NOV-2001) NIH Intramural Sec
Grovemont Circle, Gaithersburg, MD 20877,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: nisc_mouse@nhgrl.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.nisc.nih.gov
/rpt_family="ALU"
complement(51721. .51764)
/rpt_family="L1"
complement(51765. .52058)
/rpt_family="ALU"
complement(52252. .52467)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE, 4 unordered pieces
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                                                                                                                                                       Best Local Similarity Love. Matches 237; Conservative
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                                                                                                                                                     Similarity
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                     repeat_region
                                                           repeat_region
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                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                   149
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REFERENCE
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JOURNAL
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KEYWORDS
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Mus musculus nuclear factor of activated T cells c (Nfatc1) mRNA, complete cds.
AF239169.1 GI:7208617
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 3015)
Pan, S., Koyano-Nakagawa, N., Tsuruta, L., Amasakl, Y., Yokota, T.,
Mori, S., Arai, N. and Arai, K.
Molecular cloning and functional characterization of murine cDNA
encoding transcription factor NFATC
Biochem. Biophys. Res. Commun. 240 (2), 314-323 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                    * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
Insert size: 130000; agarose-fp
Insert size: 172615; sum-of-contigs
Quality coverage: 12.58x in Q20 bases; agarose-fp
Quality coverage: 9.47x in Q20 bases; sum-of-contigs
                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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                                                                                                                                                                                                                                                                                                           139 2538: contig of 2438 bp in length 439 2538: gap of unknown length 134 8133: contig of 5595 bp in length 134 8033: gap of unknown length 134 40378: contig of 32145 bp in length 1379 40478: gap of unknown length 152915: contig of 132437 bp in length 150315: contig of 132437 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .172915
/Organism="Papio cynocephalus anubis"
/db_xref="taxon:9555"
/clone="RP41-167P22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.1%; Score 48; DB 2; LA 100.0%; Pred. No. 1.1e-14; iive 0; Mismatches 0;
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40479. 172915
/note="assembly_fragment"
a 31733 c 32277 g 56096 t
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2539. 8133
/note="assembly_fragment"
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1. 2438
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Best Local Similarity 100.
Matches 48; Conservative
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2539
8134
8234
40379
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yv71e06.r1"
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32283. 32563
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complement(34737. /rpt_family="L1"
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complement(37630,
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39839, 40125
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omplement(41904.
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omplement(42942.
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18370. .48785
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complement(45672
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6100. 46516
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omplement(45964
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                                               NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of H_RG016J04;
actual end is at 156214 of H_RG016J04. The orientation of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rocte="similar to human EST T02878 (NID:g314119)"
19436. 19497
hote="similar to human EST AA123941 (NID:g1682616)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="L1"
complement(26832. .27124)
/rpt_family="ALU"
27125. .27383
/note="similar to human EST AA151807 (NID:91720502)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7125. .27544
note-"similar to human BST AA151796 (NID:g1720491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(27178. 27600)
/note="similar to human EST AA149579 (NID:91720380)
                                                                                                                                 This clone contains STS sWSS2784 (NID:\mathfrak{g}1113580) and sWSS893 (NID:\mathfrak{g}454733).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27686. .27856
/note="similar to human EST W32120 (NID:g1313113)
zb97c08.r1"
27686. .27838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(27441. .27890)
/note="similar to human EST N52554 (NID:g1193720)
yy36a11.s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Li"
complement(11315. .11984)
/rpt_family="Li"
11666. .11687
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complement(25113. .25148)
/rpt_family="L1"
complement(25561. .25578)
                                                                                                                                                                                                                                                                   /clone="RG016J04"
/clone_lib="CITB-978SK-B"
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complement(9406. .9975)
/rpt_family="L1"
complement(10000. .11285)
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/rpt_family="L1"
15715. .15767
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/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .12299
                                                                                                                                                                                    1. .156214
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                326. .621 /rpt_family="ALU" complement(977. .1499) /rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .8347)
                                                                                                                                                                  Location/Qualifiers
              Selection: chloramphenicol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (12010.
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5319, 524
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family="L1"
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27125. .275
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                                                                                                   clone is unknown.
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Direct Submission
Submitted (12-DEC-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 161001 bases at least Q40 Consensus quality: 161422 bases at least Q30 Consensus quality: 161562 bases at least Q20 Insert size: 143000; agarose-fp Insert size: 162428; sum-of-contigs Quality coverage: 10.76x in Q20 bases; sum-of-contigs Quality coverage: 9.47x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13922: contig of 13922 bp in length 14022: gap of unknown length 36248: contig of 22226 bp in length 36148: gap of unknown length 66192: contig of 29844 bp in length 66292: gap of unknown length 92168: contig of 25876 bp in length 122036: contig of 25876 bp in length 122136: contig of 29768 bp in length 122136: contig of 29768 bp in length 152136: gap of unknown length 162928: contig of 40792 bp in length
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/note-"assembly_fragment"
36349. 66192
/note-"assembly_fragment"
66293. 92168
/note-"assembly_fragment"
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/note="assembly_fragment"
122137. 162928
/note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9598"
/clone="RP43-120K11"
                                                                                                                                ----- Genome Center
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29878 c 30533 g
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vector_side:left"
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1. .13922
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                                       Green, E.D.
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Score 262; DB 2; Length 162928; Pred. No. 3.8e-127;

98.9%; S 100.0%;

Best Local Similarity

Query Match

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Primates; Catarrhini; Hominidae; Homo.
E (attung, S. and Magyl, L.
The sequence of H. sapiens BAC clone RG016J04
L (npublished (1997)
E 2 (bases 1 to 156214)
S Waterston, R.
Direct Submission
L Submitted (09-MAY-1997)
Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, Mo 63108, USA
http://genome.wustl.edu/gsc
e-mail: sapiens@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                   Db 116107 CATGCCATTATTTTATGACTTCTACGTTCAGTTACAAGTATGCTGTCAATTATTGTGG 116048
                                                                                                                                                                                                                                                                                                   DD 115987 TTTCACAAATGTCATGTTTGCCAATATGAATTTTCTAGTCAACATATTATTGTAATTTA 115928
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Gaps
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  Mismatches
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Matches 262; Conservative
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Human BAC Papio cyn

Homo sapi Human DNA

Homo sapi Canis fam Homo sapi

Human DNA Homo sapi

Word size :

Searched:

Sequence:

Run on:

Database :

Mus muscu

Human DNA Canis fam

Homo sapi Homo sapi Homo sapi

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AC097/44 EMECA
AF239169 Mus muscu
AF087606 Mus muscu
AF087434 Mus muscu
AL139219 Human DNA
AC009278 HOMO Sapi
AC027234 HOMO Sapi
                                                                                                                                                                                                                                                                                                                L05466 Pneumocysti
Ax344619 Sequence
U61945 Caenorhabdi
AC107535 Rattus no
AC106899 Mus muscu
AC10622 Homo sapi
AX251504 Sequence
AX344503 Sequence
AX344503 Sequence
AC10645 Homo sapi
AC100016 Mus muscu
AC004211 Homo sapi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC104475 162928 bp DNA linear HTG 12-DEC-2001
Pan troglodytes clone RP43-120K11, WORKING DRAFT SEQUENCE, 6
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AC091464 Mus muscu
AC02062 Mus muscu
AC079818 Mus muscu
AC170966 Pneumocys
                                                                                                               AC013742 Homo sapi
Continuation (7 of
AL035460 Human DNA
AL645757 Mus muscu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I (bases 1 to 1612928)
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffand,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haphighi,P.,
Ho,S.-L., Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-Q.,
Bedsapi,K., Maduro,Q.L., Maduro,V.B., Masiello,C., Mastrian,S.D.,
McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A., Stantripop,S.,
Thomas,J.W., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L.,
Green,E.D.
NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                            AL133323 Human DNA
AC102640 Mus muscu
AC025398 Homo sapi
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                 AL606744 M
AC108687 H
AC084099 H
                                                                                                                                                         AL360011 H
AC095026 C
AC108713 H
AC091541 C
AC068159 H
AL356356 H
AC010740 H
                                                                                            AF198614
AL592167
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AL390202_06
HS860F19
AC104475
HSAC002064
AC099742
                                         AF049606
AF087434
                               AF239169
                                                             AL139219
AC009278
AC027234
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AL592167
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AC095026
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AC068159
AL356356
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AC108687
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AC053497
AC091464
AC022062
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AF170966
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AC100899
AC010522
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AC010645
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AC025398
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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(without alignments)
1272.965 Million cell updates/sec
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                                                                                                                                     3595312
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                       1797656 seqs, 10463268293 residues
                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                       September 20, 2002, 09:57:55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                    summaries
                                                                                                                                                         OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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em_htg_inv:*
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                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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225....
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Perfect score:
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TITLE

Description

Query Match Length DB

Score

Result

Gaps

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Indels

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100.0%; Pred. No. 43; tive 0; Mismatches
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Best Local Similarity 100.
Matches 18; Conservative
  Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                    Sus scrofa
                                                                                                                                                                                                                                                                                                                                 pig.
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VERSION
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               /clone_lib="Mil_MGC_19"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="melanotic melanoma, high MDR (cell line)"
/lab_host="melanotic melanoma, high MDR (cell line)"
/lab_host="melanotic porps, site_1: XhoI: Site_2:
/note="Organ: skin, vector: pOTB7; site_1: XhoI: Site_2:
ECORI. CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites saing the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
I.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZaP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Talentricking, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.

Besign and use of two pooled tissue normalized cDNA libraries for Unpublished (2000)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

Po Box 166, Clay Center, NE 68933-0166, USA

Fat: 402 762 4396

Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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Mammalia: Eutheria: Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 143)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pcMv SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 44 c 31 g 31 t
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Pred. No. 16;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 bp mRNA linear
389764 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
B1467930
                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
  /clone="IMAGE:4869439"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Sus scrofa"
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/clone_lib="MARC 2PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGAGG
Plate: 143 row: I column: 19
Seq primer: ATTTAGGGGACACTATAG.
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/lab_host="DH108"
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Best Local Similarity 100.0%; P:
Matches 19; Conservative 0;
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Length 143;

DB 10;

8.8%; Score 18;

Query Match

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Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)

AL Unpublished (2000)

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (Dases 1 to 218)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laègreid, W.W. and Keele, J.W.
                                                                                                                                                                    EST 08-JAN-2001
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45;
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100.0%; Pred. No. 45;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38
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Job time: 8722 sec
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACKWARD: GTTTTCCCAGGCACG
Plate: 138 row: I column: 16
Seq primer: ATTTAGGTGACACTATAG.
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216 refrerecrestrif 199
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DEFINITION ACCESSION VERSION ORGANISM

KEYWORDS

SOURCE

REFERENCE AUTHORS JOURNAL

TITLE

RESULT 11 AQ345537

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1065)

S NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Emal: cgapbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Clone distribution: MGC Clone distribution at:

http://mage.llni.gov

Loation/Qualifiers

I. 1065

/organism-Homo sapiens"
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1 (Dases 1 to 1417)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="tracon:9606"
/clone="IMAGE:4182914"
/clone="ib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/tissue_type="glioblastoma with EGFR amplification"
/tab_host="longan: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo draverage insert size 1:57 kb. Constructed by Life
Average insert size 1:57 kb. Constructed by Life
1 chologies. Note: this is a NCI CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG765708 1417 bp mRNA linear EST 15-MAY-2C 602739726F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4869439 5',
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.3%; Score 19; DB 10; Length 1065; 100.0%; Pred. No. 16; tive 0; Mismatches 0; Indels
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Plate: LLCM1741 row: c column: 08
High quality sequence stop: 46.
Location/Qualifiers
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/db_xref="taxon:9606"
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BG765708.1 GI:14076361
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L Unpublished (1997)
Context GSSS: RPCIII-114M17.TJ
Context GSSS: RPCIII-114M17.TJ
Context: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 40 800 800 800
Fax: 501 800
Fax: 502 Fax: 501
Fax: 502 Fax: 502
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5', mRNA sequence.
BF337390
                                                                                                                                                                                                                                                 AQ345537 629 bp DNA linear GSS 07-MAY-1999
RECIL1-114MI7.TV RPCI-11 Homo sapiens genomic clone RPCI-11-114MI7,
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
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100.0%; Pred. No. 15;
iive 0; Mismatches 0; Indels
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/db_xref="GDB;7543696"
/db_xref="taxon:9606"
/clone="RRCI-11-114M17"
/clone_lib="RRCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
/cell_type="Lymphocytes"
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AQ345537
AQ345537.1 GI:4170433
       112 aagaaaggctggggaaaga 130
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ORGANISM

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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BASE COUNT ORIGIN

FEATURES

Matches

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EST 15-MAY-2001

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/cell_type="Sperm"
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Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are available from Research Genetics (info@resgen.com). BAC end search page:
end search page:
trp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M3-21
Class: BAC ends.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                       /clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                        /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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 Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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                         Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2185 row: E column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 12; Length 444; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                             1 others
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Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryctic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2185 Col=10 Row=E"
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/db_xref="taxon:9606"
/clone="233911"
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/sex="Male"
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100.0%; Pre
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Best Local Similarity 100.
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3868
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availablility, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1019 row: K column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ820554 linear GSS 26-AUG-1999 HS_5443_A2_F08_SPGE RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1019 Col=16 Row=K, DNA sequence.
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 551)
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                                                                                                                                                                                                                               Gaps
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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/clone_lib="RPCI-11 Human Male BAC Library"
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                                                                                                                                                                  Score 19; DB 12; Length 466;
Pred. No. 14;
Mismatches 0; Indels
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/db_xref="taxon:9606"
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100.0%; Pre
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AQ820554.1 GI:5782947
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                            HindIII"
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Query Match

Matches

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT AG024836

g

ORGANISM

REFERENCE AUTHORS

FEATURES

TITLE

REFERENCE

BASE COUNT ORIGIN

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H=2185_A2_C05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2185 Col=10 Row=E, DNA sequence. AQ063518 AQ063518 AQ063518.1 GI:3378776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p1773 vector. Library and Eco RI sites of the modified p1773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " 96 c 62 g 177 t
                                                                                                                                                                                                                               Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
, Ph.D., M. Fatima Bonaldo
, Ph.D.
                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 380 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 224.
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Cațarrhini; Hominidae; Homo.
                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
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14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1839094"
/clone=lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH108"
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AI208199.1 GI:3770141
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                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 423)
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                                                                                     Homo sapiens
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                                                             human.
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                                                                                                                                                                                                                                                                                                                                            GSS 02-MAY-2000
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Oryza sativa (sub_species:japonica, strain:NC0384,

Cultivar:Nipponbare) DNA, clone_lib:PCR product directly amplified
from rice genomic DNA clone:T2942T.

Oryza sativa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (sites)
Miyao, A. and Hirochika, H.
Rice insertion mutants
Unpublished (1999)
2 (bases 1 to 289)
Miyao, A., Miyazaaki, A., Yamashita, Y. and Hirochika, H.
Direct Submission
Submitted (25-OCT-1999) to the DDBJ/EMBL/GenBank databases. Akto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miyao, National Institute of Agrobiological Resources, Molecular Genetics; 2-1-2, Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.ip, URL:http://www.abr.affrc.go.jp/, Tel:81-298-38-7006, Fax:81-298-38-7006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Sequence group name: T29427.-The 3' end of retrotransposon Tos17 was found immediately upstream of this sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sub_species="japonica"
/db_sref="taxon:4530"
/clone="12942"
/clone_lb="PCR product directly amplified from rice genomic DNA"
                                                                                                                                                  Gaps
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Pred. No. 5;
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                                                                                                                                                                                                                                                                                                                                         289 bp
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/strain="NC0384"
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100.0%; Pre
/note="putative
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Query Match

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2444. .2449
/note="putative"
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Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:4238935"
/clone="IMAGE:4238935"
/clone=lib="NOI_CGAP_Kid14"
/lab_host="DH10B (%I phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies: Note: this is a NCI_CGAP Library. |"
244 c 231 g 245 t
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921538B17:homolog to CDNA FLJ14101 FIS, CLONE MAMMA1000859, full insert sequence.
                 Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM981 row: d column: 08
High quality sequence stop: 660.
Location/Qualifiers
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Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA,
clone_llb:RIKEN full-length enriched mouse cDNA library
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High-efficiency full-length CDNA cloning
Wath. Enzymol. 303, 19-44 (1999)
9279253
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  Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:10090"
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100.0%; Pre
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Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Aral, A.,
Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,
Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F.,
Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T.,
Kato, H., Kawali, J., Kojima, Y., Konda, M., Koya, S.,
Kurihara, C., Matsuyama, T., Myazaki, A., Nishi, K., Nomura, K.,
Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,
Salto, H., Saito, R., Saho, H., Sano, H., Sasaki, D.,
Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
Yasunishi, H., Tagami, M., Tagawa, A., Takahashi, F.,
Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemonic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MYISFCIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVA
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                                                                                                                                                             4 (sites)
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
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/note="data source:SPTR, source key:Q9H7Y1, evidence:ISS
homolog to CDNA FLJ14101 FIS, CLONE MAMMA1000859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                   Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 (bases 1 to 2473)
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/organism="Mus musculus"
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Holzman, T., Adams, M.D. and

DEFINITION

RESULT AQ236699

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ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL COMMENT

TITLE

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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Seq primer: 1100 row: O column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="watcor: pbace3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pbace3.6 vector at EcoRI sites" 5 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                             1 (bases 1 to 526)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-11 Human Male BAC Library"
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4.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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Location/Qualifiers
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AQ836131
AQ836131.1 GI:5806005
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BF784438
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                            AQ236699 579 bp DNA linear GSS 21-APR-1999
RPCIll-68C15.TK RPCI-11 Homo sapiens genomic clone RPCI-11-68C15,
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Adams, M. D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Une of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Other, GSSs: RPCI11-68C15.TJ
Contact: Mark Adams
The Institute for Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fex: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           library availability, please contact Pieter d Jong Oppererdeform and butfalo.edu. Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Class: BAC ends.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"

**RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                Gaps
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Pred. No. 1.2;
0; Mismatches 0; Indels
                                              Length 558;
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                                                 Score 30; DB 10;
                                  14.7%; Score ...
100.0%; Pred. No. 1.4e-
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                                                                                                                                                                     143 TTTATACACCACCAAACTTGTTCTTGCTC 172
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                                                                                                                                          6 tttatacaccaccaaactttgttcttgctc 35
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Matches 30; Conservative
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BASE COUNT ORIGIN

FEATURES

18 8.8 543 12 BH110402 BE031241 BE031241 129738 MA 18 8.8 633 9 AIO54511 AO739010 AO73910 AO54511 Coau0001D 18 8.8 888 12 AO745201 AO745201 <t< th=""><th>ALIGNMENTS BW431438 BW431438 1 Ducol6F03 Bos taurus Ducdenum #1 library Bos taurus cDN sequence. BW431438 EST. COW. BOS taurus BUKA31438 BUKA31438 EST. COW. BOS taurus BUKA3160 BOYINGE: BUTHERIA: CETATIONGCT/HA; Ruminantia; Pecorat BOYINGE: BOYINGE: BOYINGE: BOYINGE: BOYINGE: BOYINGE: BOYINGE: CONTACT: CONT</th></t<>	ALIGNMENTS BW431438 BW431438 1 Ducol6F03 Bos taurus Ducdenum #1 library Bos taurus cDN sequence. BW431438 EST. COW. BOS taurus BUKA31438 BUKA31438 EST. COW. BOS taurus BUKA3160 BOYINGE: BUTHERIA: CETATIONGCT/HA; Ruminantia; Pecorat BOYINGE: BOYINGE: BOYINGE: BOYINGE: BOYINGE: BOYINGE: BOYINGE: CONTACT: CONT
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: September 20, 2002, 08:33:54; Search time 5053.42 Seconds (without alignments) 544.855 Million cell updates/sec Title: US-09-802-520-8 Sequence: 1 cagagittatacaccacaagggtcacagiaatgggatga 204 Scoring table: OLIGO_NUC Gapop 60.0, Gapext 60.0 Searched: 13736207 seqs, 6748477542 residues Word size: 0 Total number of hits satisfying chosen parameters: 27472414 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Listing first 45 summaries	BST:* EST:* EST:

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          TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE NUMBER OF SEQUENCES: 83
CORRESPONDENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Avenue, NW, suite 5500 CITY: Washington STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTRY: USA
ZIP: 20006-1888
COMPUTRY: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,357
FILING DATE: 08/918,288
FILING DATE: 23 AUG-1997
APPLICATION NUMBER: 08/853,524
FILING DATE: 18 FEB-1994
ATTORNEY/AGENT INFORMATION:
NUMBER: 08/199,382
FILING DATE: 18 FEB-1994
ATTORNEY/AGENT INFORMATION:
NUMBER: 29/959
REGISTRATION NUMBER: 29/959
REGISTRATION NUMBER: 29/959
REGISTRATION NUMBER: 29/959
REGISTRATION NUMBER: 29/959
REEEPRONEE/DOCKET NUMBER: 29/959
TELECOMMUNICATION INFORMATION:
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TELEFRENCE. 202-887-10763
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TELEX:
SOUGHOUS FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 base pairs
TYPE: nucleic acid
STRANDENNES:
APPLICANT: MOYLE, William R.
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TOPOLOGY:
US-09-282-357-28
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Search completed: September 20, 2002, 09:51:18 Job time: 11866 sec

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8.3%; Score 17; DB 4; Length 693;
                                                                                Indels
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Patent No. 6238890
GENERAL INFORMATION IFVING
APPLICANT: BOIME, William R
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
CORRESPONDENCE: 83
CORRESPONDENCE: MORNISON & FORENTER
ADDRESSES: MORNISON & FORENTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SUFTWARE: FastEND for Windows Version 2.0
SUBTENT APPLICATION DATE:
APPLICATION NUMBER: US/08/918,288
                                        Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. ...
                                                                                Mismatches
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FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/282,357
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28, Application US/09282357
Patent No. 6242580
GENERAL INFORMATION:
APPLICANT: BOIME, Irving
100.08; P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Wind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                184 agggtcacagtaatggg 200
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SEQUENCE CHARACTERISTICS:
LENGTH: 693 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                             87 AGGGTCACAGTAATGGG 71
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Best Local Similarity 100.'
Matches 17; Conservative
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                                   Best Local Similarity 100.
Matches 17; Conservative
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CITY: Washington
STATE: DC
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-08-918-288-28/c
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100.0%; Pred. No. 2.1;
ive 0; Mismatches 0; Indels
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STREET: 2000 Pennsylvanla Avenue, NW, suite 5500
CITX: Washington
STATE: DC
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Sequence 31, Application US/09282357
Patent No. 6242580
GENERAL INFORMATION:
APPLICANT: BOIME, Irving
APPLICANT: MOYLE, William R.
TITLE OF INVENTION: GINGLE-CHAIN FORMS OF THE
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 150 COMPUTER: 50 COMPUTER: 150 COMPUTER: 50 COM
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REFERENCE/DOCKET NUMBER: 29500-20050.25
                               TELECOMMUNICATION INFORMATION: TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
                                                                                                                                                                                                        31:
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                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 AGGGTCACAGTAATGGG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 17; Conservative
                                                                  TELEPHONE: 202-887-15/
TELEFAX: 202-887-0763
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TELEFAX: 202-887-0763
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US-08-918-288-31
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Length 681;

8.3%; Score 17; DB 4;

Query Match

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GENERAL INCORNATION:
APPLICANT: Robert 2. Florkiewicz
APPLICANT: Andrew Baird
APPLICANT: Andrew Baird
APPLICANT: Dale E. Warnock
TITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING THE SAME
TITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING THE SAME
FILE REPERENCE: 200124 402C4
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2: MORRISON & FOERSTER
2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/08918288
Patent No. 6238890
GENERAL INFORMATION:
APPLICANT: BOINE, Irving
APPLICANT: MOYLE, William R.
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,288
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Pred. No. 2;
0; Mismatches
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ATTORNEY_AGENT INFORMATION:
NAME: MUTAS hige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/282,357
                                                                                                                                            Sequence 4, Application US/09451905
Patent No. 6306613
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Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
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                          271 AGGGTCACAGTAATGGG 287
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ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 09-MAY APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien
US-09-451-905-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2000 Pen
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: DC
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                                                                                                     RESULT 11
US-09-451-905-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Florkiewicz, Robert Z.
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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100.0%; Pred. No. 2;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORMY:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Maki, David J.

REGISTRATION UNDRER: 31,392
REFERENCE/DOCKET NUMBER: 200124.401D1
TELECOMMUNICATION INFORMATION:
TELEFONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/466,036A FILING DATE: 17-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                              8.3%; Score 17; DB 100.0%; Pred. No. 2; Live 0; Mismatches
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APPLICATION NUMBER: US 09/211,290
FILING DATE: «UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-466-036A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09466036A
Patent No. 6281197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
STATE: Washington
TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                          LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.0
Matches 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                  1..348
                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-09-322-676-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-466-036A-4
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(206) 622-4900
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TYPE: nucleic acid
STRANDEDNESS: single
            Washington
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US-09-030-613-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-322-676-4
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                                                                                                                                                                               Sequence 4, Application US/09211290
Patent No. 60/1885
GENERAL INFORMATION:
APPLICANT: Florkiewicz, Robert Z.
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Scattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09030613
Patent No. 6083706
GENERAL INFORMATION:
APPLICANT: Florkiewicz, Robert Z.
APPLICANT: Baird, J. Andrew
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 351
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,290
FILING DATE: 12-DEC-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17; DB 3;
Pred. No. 2;
0; Mismatches
              Pred. No. 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200124.401D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY FACENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 20012
RELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
100.0%; Fr. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; P:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 AGGGTCACAGTAATGGG 287
                                                               184 agggtcacagtaatggg 200
                                                                             271 AGGTCACAGTAATGG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.3
Best Local Similarity 100.
Matches 17; Conservative
            Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
US-09-211-290-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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COMPUTER REALABLE FORM:

COMPUTER IN TPE: Floppy disk
COMPUTER: 1916
COMPUTER: 11 PPE: Compatible
CASSITENCENTON NUMBER: 39,317
FALLMEN DATE: NUMBER: 39,317
FALLMEN DATE: COMPATION: FREE: 1998
FATTOREY AMENT INVORMATION: Carol
RESTRANCONCENT NUMBER: 39,317
FATTOREY AMENT INVORMATION: Carol
RESTRANCONCENT NUMBER: 39,317
FATTOREY CAROL
TELEGOMENICATION INFORMATION: Carol
RESTRANCONCENT NUMBER: 39,317
FATTOREY MACHINE: 2006
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Patent No. 5891855
GENERAL INFORMATION:
APPLICANT: Florkiewicz, Robert Z.
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 351;
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ZIP: 98104-7092
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DEACHLIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,895
FILING DATE: 31-JAN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5891855tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100,416
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION POR SEQ ID NO: 4:
CENTIFICE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.3%; Score 17; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17; DB 4;
Pred. No. 2;
0; Mismatches
                                                                                                                                                 29,959
3R: 29500-20050.25
                     APPLICATION NUMBER: 08/199,382 FILING DATE: 18-FEB-1994 ATTORNEY/AGENT INFORMATION: NAME: Murashige, Kate H REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.3%; Scc.
100.0%; Pre
0;
                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELERAX: 202-887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 351 base pairs
nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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US-08-599-895-4
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US-09-282-357-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-599-895-4
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2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARȚET NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS: ADDRESSE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Avenue, NW, suite 5500 CITY: Washington
                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/918,288 FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 2; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29500-20050.25
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                                                                                                                                                                                                                                                                                                                         APPLICATION TO STATE THE STATE OF STATE
                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/282,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34, Application US/09282357
Patent No. 6242580
GENERAL INFORMATION:
APPLICANT: BOIME, Irving
APPLICANT: MOYLE, William R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
PRIOR APPLICATION DATA:
08/918,288
PILING DATE: 25 AUG-1997
APPLICATION NUMBER: 08/853,524
                                                   MEDIUM TYPE: Diskette COMPUTER: IBM COMPAtible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.3°
Best Local Similarity 100°.
Matches 17; Conservative
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ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
20006-1888
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US-08-918-288-34
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                                                                                                  ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
                      SINGLE-CHAIN FORMS OF THE GLYCOPROTEIN HORMONE QUARTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/08918288
Patent No. 6238890
GENERAL INFORMATION:
APPLICANT: BOING: Irving
APPLICANT: MOYLE, William R.
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
                                                                                                                                                                                                                                                                       OPETITIES IN COMPATION OF CONTROLLER OF STEMEN DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,357
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/918,288
FILING DATE: 25 AUG-1997
APPLICATION NUMBER: 08/918,288
FILING DATE: 1990
APPLICATION NUMBER: 08/919,382
FILING DATE: 18-FEB-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: MUTSABLIGE, NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.3%; Score 17;
100.0%; Pred. No.
ive 0; Mismatcl
    MOYLE, William R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 312 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 agggtcacagtaatggg 200
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
                                                             NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Coding S
LOCATION: 1...303
CTHER INFORMATION:
US-09-282-357-32
                      TITLE OF INVENTION:
                                                                                                                                                                                 COUNTRY: USA
ZIP: 20006-1888
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                                                                                                                                                             STATE:
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                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: BOIME, Irving
APPLICANT: MOYLE, William R.

TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY AGENT INFORMATION:
NAME: MITASALIGE, Kate H
REGISTRATION NUMBER: 29,959
REFERCE/DOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURTENER PEPLICATION DATA:
APPLICATION NUMBER: US/08/918,288
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Mismatches
420 TTTATACACCACAAACTTGTTCTTGCTC 449
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/282,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/09282357
Patent No. 6242580
GENERALINFORMATION:
APPLICANT: BOIME, ITVING
                                                                                                                      Sequence 32, Application US/08918288
Patent No. 6238890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08; FIX
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                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 bases pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 agggtcacagtaatggg 200
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 202-887-15
TELEFAX: 202-887-0763
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: US-08-918-288-32
                                                                                                                                                                                                                                                                                                                                    Washington
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                             USA
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US-09-282-357-32
                                                                               RESULT 2
US-08-918-288-32
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Title: Perfect score:

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APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STRATE: CALIFORNIA
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
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1.1e-07;
US-08-918-288-26
US-09-282-357-26
US-08-918-288-16
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US-09-282-357-16
US-08-918-288-11
US-08-918-288-5
US-08-918-288-5
US-08-918-288-5
US-09-282-357-5
US-09-282-357-5
US-09-282-357-5
US-09-282-357-5
US-09-282-357-20
US-09-282-357
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NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0527 US
TELECOMUNICATION INFORMATION:
TELECHONE: (650) 855-0555
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1213 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
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APPLICATION NUMBER: US/09/083,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09083521 Patent No. 6048970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; IMMEDIATE SOURCE:
LIBRARY: PROSTUT10
; CLONE: 1691243
US-09-083-521-3
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                                                                                                                                                                                                                                                                                                                 ; Search time 139.75 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Compugen Ltd
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US-09-030-613-4
US-09-322-676-4
US-09-466-036A-4
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US-08-918-288-28

US-09-282-357-28

US-08-918-288-13

US-09-282-357-13

US-09-282-357-13

US-09-282-357-29
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US-08-918-288-10
US-09-282-357-10
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US-08-918-288-33
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                                                       GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                         nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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Score

Result No.

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cc stimulating hormone (FSH). FSH is a heterodimeric gonadotropic hormone cc secreted by the pituitary gland. It consists of two subunits, referred cc to as alpha and beta. The protein is used to produce compositions of the invention. The specification describes a stabilized dry powder composition for delivery of a FSH to the deep lung of a mammalian cc subject. The compositions promotes ovarian follicular development. The cc composition is useful for treating female infertility.

Sc sequence 273 BP; 74 A; 73 C; 62 G; 64 T; 0 other;

Sc sequence 273 BP; 74 A; 73 C; 62 G; 64 T; 0 other;

Autches 17; Conservative 0; Mismatches 0; Indels 0; Gaps:

Autches 17; Conservative 0; Mismatches 0; Indels 0; Gaps:

Outlies agggtcacagtaatggg 200

196 agggtcacagtaatggg 212
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Search completed: September 20, 2002, 09:59:59 Job time: 11717 sec

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DNA encoding an alpha subunit variant of a follicle stimulating hormone.
                                                                                                                                                                                                     The present sequence encodes an alpha subunit variant of a follicle stimulating hormone (FSH). FSH is a heterodimeric gonadotropic hormone secreted by the pituitary gland. It consists of two subunits, referred to as alpha and beta. The protein is used to produce compositions of the invention. The specification describes a stabilized dry powder composition for delivery of a FSH to the deep lung of a mammalian subject. The compositions promotes ovarian follicular development. The composition is useful for treating female infertility.
                                                                                            Stabilized dry powder composition for delivery to the deep lung comprising follicle-stimulating protein (FSP) and an excipient, useful for the treatment of female infertility -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stabilized dry powder composition for delivery to the deep lung comprising follicle-stimulating protein (FSP) and an excipient, useful for the treatment of female infertility -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes an alpha subunit variant of a follicle
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Allen DL, Hughes BL, Stiff-Torvik M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 270 BP; 74 A; 71 C; 62 G; 63 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                8.3%; Score 17; DB 21;
100.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No. 30; ive 0; Mismatches
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                                                                                                                                                                         Disclosure; Page 108; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 108; 125pp; English
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99US-0130099
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Matches 17; Conservative
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Venthoye G,
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    Roeder WD;
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Stults CLM, Venthoye
Wolff RK, Roeder WD;
                                      WPI; 2000-647398/62.
P-PSDB; AAB19374.
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20-APR-1999;
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  Wolff RK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC61707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding an alpha subunit variant of a follicle stimulating hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes an alpha subunit variant of a follicle stimulating hormone (FSH). FSH is a heterodimeric gonadotropic hormone secreted by the pituitary gland. It consists of two subunits, referred to as alpha and beta. The protein is used to produce compositions of the invention. The specification describes a stabilized dry powder composition for delivery of a FSH to the deep lung of a mammalian subject. The compositions for mammalian follicular development. The composition for treating female infertility.
                                                                                                                                                                                                                                                                                                                           Stabilized dry powder composition for delivery to the deep lung comprising follicle-stimulating protein (FSP) and an excipient, useful for the treatment of female infertility -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                           Chiang H;
Stiff-Torvik M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bennett DB, Greene J, Chiang H;
Allen DL, Hughes BL, Stiff-Torvik M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Length 267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Follicle stimulating hormone; FSH; gonadotropic hormone; ovarian follicular development; infertility; ss.
                                                                                                                                                                                           Bennett DB, Greene J,
Allen DL, Hughes BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 267 BP; 73 A; 71 C; 61 G; 62 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; DB 2
Pred. No. 30;
0; Mismatches
                                                                                                                                   (INHA-) INHALE THERAPEUTIC SYSTEMS INC. (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INHA-) INHALE THERAPEUTIC SYSTEMS INC. (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 108; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.3%; Scc.
100.0%; Pre
0; '
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99US-0130099.
                                      13-APR-2000; 2000WO-US09869
                                                                          99US-0129121
99US-0130099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC61708 standard; DNA; 270
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                                                                                                                                                                                         Nagarajan S, Patton JS,
Stults CLM, Venthoye G,
Wolff RK, Roeder WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Conservative
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Stults CLM, Venthoye G,
                                                                                                                                                                                                                                                                    WPI; 2000-647398/62.
P-PSDB; AAB19375.
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                                                                          13-APR-1999;
20-APR-1999;
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20-APR-1999;
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19-OCT-2000
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a Also included are vectors and host cells expressing the proteins, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign or prostatic hyperplasia, acute prostatils, testicular cancer, benign cryptorchidism, undescended, retractile, ascending or vanished testis. Other prolliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast concer, parent concer, breast concer, parent cancer, process.
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                                                                                                                                                                                                                                                                                                                                               New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Six-Transmembrane Protein of Prostate 1, STMP1, exon 6/3' UTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence represents the open reading f x \bar{a} m e of a prostate specific protein, Six-Transmembrane Protein of Prostate 1, STMP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4329;
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100.0%; Pred. No. 3.6e-06;
iive 0; Mismatches 0;
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                                                                                       Location/Qualifiers
178..1650
/*tag= a
                                                                                                                            /product= "STMP1"
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Fig 4D; 114pp; English.
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                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09410
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Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                          (SAAT/) SAATCIOGLU F.
                                                                                                                                                                                                                                                                                                           WPI; 2001-662926/76.
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                                                                                                                                                     WO200172962-A2
                                                                                                                                                                                                                                                                                    Saatcioglu F;
                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2002
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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, artibodies against the transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules of for nucleic acids and mathods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, banign prostatic hyperplasia, acute prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished creatis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The
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benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorochidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ds; exon 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
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100.0%; Pred. No. ...
"... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09410.
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Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SAAT/) SAATCIOGLU F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-662926/76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saatcioglu F;
                                                                                                                                                                                             Homo sapiens.
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (I) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques or restore normal activity of (II) susful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and anino acid sequences. AAS64197-AAS94564 represent novel human DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORF of Six-Transmembrane Protein of Prostate 1, STMP1.
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2000US-0649167.
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P-PSDB; ABG00113.
                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
                                                                                                                           WO200175067-A2
                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                      31-MAR-2000;
23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New STEAP (six transmembrane epithelial antigen of the prostate) proteins, expressed in human cancers, useful for detecting and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Faris M;
/product= "Human six transmembrane epithelial antigen of the prostate (STEAP)-2, alternative version"
/note= "CDS does not include start and stop codon"
/transl_except= (pos:1714..1722, aa.Asp.Ala)
/transl_except= (pos:1834..1842, aa.Asp.Ala)
/transl_except= (pos:1857..1965, aa.ful-01y)
/transl_except= (pos:2050..2058, aa.ful-ser)
/transl_except= (pos:2060..2058, aa.ful-ser)
/fransl_except= (pos:2062..2070, aa.Asn-Phe)
/note= Inframe stop codon alters the reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The present sequence is also shown in sequence listing of the specification, but it lacks nulceotides at its 5^{\prime} end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Afar DEH, Hubert RS, Raitano AB, Saffran DC, Mitchell SC, Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2453 BP; 648 A; 537 C; 520 G; 748 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding novel human diagnostic protein #104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.7%; Score 30; DB 22; I
100.0%; Pred. No. 3.6e-06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1631 tttatacaccaccaaactttgttcttgctc 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 tttatacaccaccaaactttgttcttgctc 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Fig 9A-9D; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS64300 standard; cDNA; 3900
                                                                                                                                                                                                                                                                                                                                                                 06-DEC-2000; 2000WO-US33040
                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0455486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAE02781, AAE02841.
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                                                                                                                                                                                                                    /partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UROG-) UROGENESYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-367804/38.
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                         WO200140276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    06-DEC-1999;
                                                                                                                                                                                                                                                                                                                    07-JUN-2001
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Gaps

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Indels

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Length 3900;

Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer;

AAS64300;

DNA

RESULT 10

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AAS64300

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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them.
Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign of the testis or prostate practicularly prostate cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence represents the second open reading frame of a prostate specific protein, Six-Transmembrane Protein of Prostate 1, STMPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human six transmembrane epithelial antigen of prostate-2 clone GTD3 cDNA.
                                                                                                                                                                                      New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/product= "Human six transmembrane epithelial antigen
/product= "Forestate (STEAP)-2"
709..2073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, cytostatic, antiproliferative, vaccine, gene therapy, six transmembrane epithelial antigen of the prostate-2; STEAP-2; chromosome 7q21; cancer; prostate; colon; bladder; lung; ovarian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2238 BP; 607 A; 457 C; 453 G; 721 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 22; I
Pred. No. 3.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "Kozak region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.7%; Sc...
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                           Claim 5; Fig 4G; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD07072 standard; cDNA; 2453
 23-MAR-2001; 2001WO-US09410.
                                 24-MAR-2000; 2000US-191929P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                      WPI; 2001-662926/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 30; Conserv
                                                                   (SAAT/) SAATCIOGLU
                                                                                                                                                        P-PSDB; AAU10188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pancreatic; ss.
                                                                                                    Saatcioglu F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORF2 of Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.7%; Score 30; DB 23; Length 21 100.0%; Pred. No. 3.6e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2192 BP; 559 A; 507 C; 551 G; 575 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                  Claim 1; SEQ ID No 12297; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1406 tttatacaccaccacatttgttcttgctc 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "STMP1, ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 tttatacaccaccaaactttgttcttgctc 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS15810 standard; cDNA; 2238
Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Liu C,
                            WPI; 2001-639362/73
                                               P-PSDB; ABG12306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W0200172962-A2
                                                                                                                                    biodiversity
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Drmanac RT,
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AAS15810

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Length 2238; Indels

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23-MAR-2001; 2001WO-US09410.
                                  24-MAR-2000; 2000US-191929P
                                                                                                        WPI; 2001-662926/76.
                                                          (SAAT/) SAATCIOGLU
                                                                                                                     P-PSDB; AAU10187
                                                                                  Saatcioglu F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS76493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them.

Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis other proliferative disorders for which the modulators may be testis other proliferative disorders for which the modulators may be caucer, panoreatic cancer, liver cancer and lung cancer, breast cancer, panoreatic cancer, liver cancer and lung cancer. The
                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ds.
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             **tag= b
note= "Represents 12713 nucleotides of intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= f
/note= "Represents 2299 nucleotides of intron 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= d
note= "Represents 1396 nucleotides of intron 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag= e
hote= "Represents 2372 nucleotides of intron 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
"Represents 338 nucleotides of intron 1"
                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human DNA for Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                           14.7%; Score 30; DB 22; Length 1680;
                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                        Sequence 1680 BP; 467 A; 334 C; 373 G; 506 T; 0 other;
                                                                                                                                                                                                                                                                                         Pred. No. 3.6e-06;
                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                        1454 tttatacaccacaactttgttcttgctc 1483
                                                                                                                                                                                                                                                                                                                         6 tttatacaccaccaaactttgttcttgctc 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                              14., ...
100.0%; Fie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product= "STMP1"
           Claim 4; Fig 4E; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          AAS15793 standard; DNA; 1725 BP
                                                                                                                                                                                                                  Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     00..1702
                                                                                                                                                                                                                                                                                                   30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1410
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAS15793;
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the protein, antibodies against the proteins. Compounds that modulate the prostating modulators of the croteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign or prostatic hyperplasia, acute prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be testis. Other proliferative disorders for which the modulators may be cancer, pancreatic cancer, liver cancer and lung cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence encodes a prostate specific protein, Six-Transmembrane
New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1725 BP; 476 A; 340 C; 387 G; 517 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #12297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30; DB 22;
Pred. No. 3.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.7%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 4B; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS76493 standard; cDNA; 2192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein of Prostate 1, STMP1
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2000US-0649167
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Best Local Similarity 100.
Matches 30; Conservative
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23-AUG-2000;
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Saatcioglu F;
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                                                                                                                                                                                                                 Protein
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                                                                                                                                                                                                                                                                                                                                                                                RESULT
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                    This sequence represents CDNA encoding human prostate growth-associated protein PGAMP-1. Nucleotides encoding PGAMP-1 were initially identified in a prostate cDNA library, this sequence representing a consensus. Human prostate growth associated membrane proteins PGAMP-1 and PGAMP-2 (AAY52590) may be used to raise specific antibodies and to screen for specific modulators (agonists, antagonists or other potential therapeutic agents). Antagonists of PGAMP are used to treat or prevent wide range of cancers (solid tumours, leukaemia, lymphoma etc.) and represented sisorial syndrome, prostatitis). PGAMP-encoding nucleic acids, its fragments and complements, may be used for recombinant production of PGAMP proteins, in gene therapy (e.g., as antisense melecules, triplexforming molecules and ribozymes), and as diagnostic probes and primers. Committing molecules may be used for diagnosis and monitoring of antagonists (including targetted delivery of other drugs), and in competitive drug screens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular aancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA encoding ORF2 of Six-Transmembrane Protein of Prostate 1.
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                                                                                                                                                                                                                                                                        Length 1213;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                      Sequence 1213 BP; 335 A; 239 C; 215 G; 424 T; 0 other;
                                                                                                                                                                                                                                                                       14.7%; Score 30; DB 21; I
100.0%; Pred. No. 3.6e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; cytostatic; ss; ORF2
                                                                                                                                                                                                                                                                                                                    /product= "STMP1, ORF2"
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188..1552
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Claim 7; Page 67; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                     AAS15811 standard; cDNA; 1561
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                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                   Local Similarity
tes 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; lung
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                                                                                                                                                                                                                                                                        Query Match
Best Local S
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                                                                                                                                        transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, cancer, percent and lung cancer. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorochidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic, cancer; liver cancer; lung cancer; cytostatic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate specific protein, Six-Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                          The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA encoding Six-Transmembrane Protein of Prostate 1, STMP1.
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Pred. No. 3.6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Prostate 1, STMP1, ORF2.
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100.0%; Prec
0; M
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Claim 4; Fig 4H; 114pp; English.
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Best Local Similarity
Matches 30; Conserv
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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them.

Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostaticitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished cryptorchidism, undescended, retractile, ascending or vanished used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer, the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, pressent sequence represents partial exon 6 sequence of a prostate
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New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids -
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                                                                                                                                                                                                                                                                                                                                                                                                                                       specific protein, Six-Transmembrane Protein of Prostate 1, STMP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 148 BP; 36 A; 29 C; 26 G; 57 T; 0 other;
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live 0; Mismatches
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                                                                             Claim 6; Fig 4C; 114pp; English.
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Matches 30; Conserv
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AAS15808
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testis-specific polypeptides and the nucleic acids encoding them.
Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatics, testicular cancer, benign prostatic hyperplasia, acute prostatics, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The cancer according or present sequence represents each of of a prostate specific protein, six Transmembrane protein of Prostate 1, STMP1, alternatively
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                                                                                                                            disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polycystic ovarian syndrome; prostatitis; recombinant expression; gene therapy; antisense therapy; ribozyme; diagnosis; diagnosis; monitoring; immunoassay; targetting; drug delivery; drug screening; ds.
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                                                                                                                                                                                                                                                                                                                                                                     Length 148;
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                                                                                                                                                                                                                                                                                                                  Sequence 148 BP; 36 A; 29 C; 26 G; 57 T; 0 other;
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Pred. No. 3.5e-06;
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100.0%; Pre
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                                         30; Conservative
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                                                                                                                                                                                                                                                                                  spliced version, ORF2
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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September 20, 2002, 09:59:56; Search time 600.75 Seconds (without alignments) 583.022 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                    1736436 seqs, 858457221 residues
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Gapop 60.0 , Gapext 60.0
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SIDSI/gggdata/hold-geneseq/geneseqn-embl/NA1990_DAT:*

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SIDSI/gcgdata/hold-geneseqn-embl/NA1993_DAT:*

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Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human Six-Transmem	Human Six-Transmem	Human prostate gro	Human cDNA encodin	Human cDNA encodin	Human DNA for Six-	DNA encoding novel	Human ORF2 of Six-	Himan six transmem
SUMMARIES	ΙD	AAS15799	AAS15808	AA246296	AAS15811	AAS15802	AAS15793	AAS76493	AAS15810	AAD07072
		22	22	21	22	22	22	23	22	22
	Query Match Length DB	148	148	1213	1561	1680	1725	2192	2238	2453
æ	Query Match	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7
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24-MAR-2000; 2000US-191929P.

(SAAT/) SAATCIOGLU F.

WPI; 2001-662926/76.

Saatcioglu F;

DNA encoding novel Human ORF of Six-T Human Six-Transmem DNA encoding an all DNA encoding an all DNA encoding the a DNA encoding the a DNA encoding the a	ectide se ectide se dotropin n single encoding n single n anterio	Human chorionic go Human cDNA encodin Human secreted pro C glutemicum codin Engineered human a Dimeric glycoprote Human chorionic go Human single chain Aspergillus oryzae Human single chain	
AAS64300 AAS15801 AAS15800 AAC61709 AAC61708 AAC61708 AAC61686	AAZ45449 AAZ45450 AAT03237 AAD08805 AAS08505 AAD08806 AAH46590 AAH46590	AAA53565 AAS17402 AAC00111 AAH65154 AAQ10075 AAQ1075 AAZ31747 AAD08804 AAF13416	AAD08792 AAT03236 AAT0336 AAD0803 AAD08798 AAD08798 AAD08790 AAD08790 AAT03235
23 22 21 21 21 21 21	22 22 22 22 18	22 22 22 22 22 22 22 22	555 555 555 555 555 555 555 555 555 5
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ALIGNMENTS

Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorochidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ds; exon 6. Human Six-Transmembrane Protein of Prostate 1, STMP1, partial exon 6. AAS15799 standard; DNA; 148 BP. 23-MAR-2001; 2001WO-US09410. 16-JAN-2002 (first entry) WO200172962-A2. Homo sapiens 04-0CT-2001. AAS15799; RESULT AAS15799

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Search completed: September 20, 2002, 09:57:55 Job time: 13333 sec

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Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Ho, S.-L., Idol, J.W., Karlins, E., Lee-Lin, S.-Q., Legaspi, R., Lim, M., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Snyder, B., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Green, E.D.
Direct Submission
Submitted (04-JUL-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
----------------- Genome Center
Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 225678 bases at least 040
Consensus quality: 225678 bases at least 030
Consensus quality: 225697 bases at least 030
Insert size: 256000; pulse-field-gel
Insert size: 225000; pulse-field-gel
Insert size: 126944; sum-of-contigs
Quality coverage: 11.02x in 020 bases; pulse-field-gel
Quality coverage: 12.84x in 020 bases; sum-of-contigs
                                                                                                 Gaps
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Mus musculus chromosome 5 clone RP23-261D18 strain C57BL6/J,
WORKING DRAFT SEQUENCE, 3 unordered pieces.
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pulse-field-gel
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* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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                                        Length 205085;
                                                                                            0; Indels
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                                           Score 20; DB 2;
Pred. No. 2.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: NISC
Web Site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: qv
Center clone name: 261D18
                                                                                                                                                                                                                                                                                                                                                                                                               AC092404.1 GI:14595778
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                   DD 196162 CGAAAGCTAAAACGAATTAA 196181
                                           Query Match 9.8%; Scc
Best Local Similarity 100.0%; Pi
Matches 20; Conservative 0;
                                                                                                                                          94 cgaaagctaaaacgaattaa 113
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109656
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AC092404/c
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5HGC-103088 Human Homo sapiens STS genomic, sequence tagged site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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94 degrees C for 30 seconds
60 degrees C for 30 seconds
72 degrees C for 23 seconds
30
Perkin Elmer 9700
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5801
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: AGTTGGAGTGAACGATAAACGA
Primer B: TTCAGGGTGAAACCTTCTAGCAC
STS size: 300
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.8%; Score 20; DB 2; Length 227144; 00.0%; Pred. No. 2.8;
6 227144: contig of 117389 bp in length.
Location/Qualifiers
1. .227144
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0.07 units/ul
5 ul
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/clone_lib="RPCI mouse BAC library 23"
1. .26708
/note="assembly_fragment
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9.88; Pred. No. 2.8
Best Local Similarity 100.08; Pred. No. 2.8
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Total Vol:
                                                           /organism="Mus musculus"
                                                                   /strain="C57BL6/J"
/db_xref="taxon:10090"
/chromosome="5"
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Annealing:
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us-09-802-520-8.rge

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/clone="RP23-119M19"
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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Blakesley, R.W., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Lee-Lin, S.-G., Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W.,
                                                                  /note="This clone overlaps CTD-2165P21 AC025270,
RP11-302D8 AC072032 and RP11-456H13 AC091245. Data from
overlapping BACs were added and the consensus sequence
determined from RP11-292P13 to the extent possible."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-MAR-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L. 
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Δυσυάς bp DNA linear HTG 27-C Mus musculus chromosome 5 clone RP23-119M19 strain C57BL6/J, WORKING DRAFT SEQUENCE, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Oct 27, 2001 this sequence version replaced gi:7321458
Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                             9.8%; Score 20; DB 9; Length 199503; 100.0%; Pred. No. 2.8; tive 0; Mismatches 0; Indels 0
                                                                                                                                                        Anotes overlap with CTD-2165P21, AC025270" 58018. 199503

/notes overlap with RP11-456H13, AC091245" 7240. 72280

/notes low quality data" 102297 199503

/notes overlap with RP11-302D8, AC072032" 118860. 118876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid; n/a; 100% of reads
                                                   /clone_lib="RPCI human BAC library 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                 /note="low quality data"
118943. 118945
/note="low quality data"
42859 c 41648 g 57283 t
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Center clone name: 119M19
                                   /clone="RP11-292P13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT
/chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 68341 AAGAAAGGCTGGGGAAAGAG 68360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 aagaaaggctggggaaagag 131
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                                                                                                                                             1. .41260
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Best Local Similarity 100.
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AC026813
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Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990119 Consensus quality: 199516 bases at least Q40 Consensus quality: 200596 bases at least Q30 Consensus quality: 201000 bases at least Q20 Insert size: 197000; agarose-fp Insert size: 197000; pulse-field-gel Insert size: 204185; sum-of-contigs Quality coverage: 9.56x in Q20 bases; pulse-field-gel Quality coverage: 9.66x in Q20 bases; pulse-field-gel Quality coverage: 9.03x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                              pulse-field-gel
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unknown length
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unknown length
of 13777 bp in length
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unknown length
of 19679 bp in length
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unknown length
of 5025 bp in length
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of 28030 bp in 1
t unknown length
of 43216 bp in 1
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40716 c 41296 g 61026
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/note="assembly_fragment"
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'note="assembly_fragment"
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/note="assembly_fragment"
62111. .81789
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81890. 109919
/note="assembly_fragment"
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153336. .205085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9654. .22746
/note="assembly_fragment"
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/strain="C57BL6/J"
/db_xref="taxon:10090"
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Gaps

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS

LOCUS DEFINITION RESULT 11

AC091245

ACCESSION

VERSION KEYWORDS

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Submitted (22-DEC-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA
of Washington, PO BOX 357730, Seattle, WA 98195, USA
3 (bases 1 to 199503)
Sowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,
Pate,D. and Hood,L.
Direct Submission
Submitted (12-SEP-2001) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC018901 199503 bp DNA linear PRI 12-SEP-2001
Homo sapiens chromosome 15 clone RP11-292P13 map 15q15, complete
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1 (bases 1 to 199503)

1 (bases 1 to 199603)

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Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dackhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M.P., Ratcliffe, A., Shaffer, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Sep 12, 2001 this sequence version replaced gi:13569966
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100.0%; Pred. No. 2.8;
tive 0; Mismatches 0; Indels 0;
162193. 162194

/note="low quality data"

162880. 194311

/note="overlap with CTD-2014N11, AC090888"

188555. 188632

/note="low quality data"

57675 a 40759 c 40302 g 55575 t
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
AC018901
AC018901.8 GI:15559174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 aagaaaggctggggaaagag 131
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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REFERENCE
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                                                                                                                                                AC091245 194311 bp DNA linear PRI 27-OCT-2001
Homo sapiens chromosome 15 clone RP11-456H13 map 15q15, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-APR-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (27-0CT-2001) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
98105, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_in="RP11-456H13"
/clone_in="RP11-456H13"
/clone_in="RP11-456H13"
/note="This clone overlaps RP11-292P13 [Ac018901 and Ac087828], RP11-302D8 Ac072032 and CTD-2014N11 Ac090888. Data from overlapping BACs were added and the consensus sequence determined from RP11-456H13 to the extent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 194311)
Rowen, L., Madan, A., Oln, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D. and Hood, L.
Sequencing of human chromosome 15 D15S146-D15S117 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 194311)
Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,
Pate,D. and Hood,L.
Direct Submission
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Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,

Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R.,

Pate, D. and Hood, L.
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On Oct 27, 2001 this sequence version replaced gi:13569969.
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Center code: UWMSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen@systemsbiology.org
Sequencing vector: pUC18; LO8752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
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/hote="overlap with RP11-302D8, AC072032"
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AC091245.2 GI:16506376
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TITLE JOURNAL

COMMENT

FEATURES

'clone_lib="RPCI-11 Human Male BAC"

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consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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of 1498 bp in length
100 bp
of 1092 bp in length
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of 1889 bp in length
100 bp
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42963 167907: contig of 24945 bp in length
67908 168007: gap of 100 bp
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114104: contig of 19368 bp in length
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142862: contig of 28658 bp in length
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of 1059 bp in length
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f 1332 bp in length
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f 1237 bp in length
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19913: contig of 3(
4 20013: gap of 10
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1 23339: gap of 100
2510: contig of 32.
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10787: contig of
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12735: contig of
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91: contig of
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189 1247: contig of 248 1347: gap of 10
348 1956: contig of
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14917;
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8118: gap of
9450: con
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3554: cc
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6735: c
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                                       ector_side:left"
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Best Local Similarity 100.
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FEATURES Source

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ALE Dipublished

Barna, W. Bastlen, C., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, N., Bastlen, Y., Boquslavkiy, L., Boukhalter, B., Brown, A., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Glade, S., Goyette, M., Graham, L., Grand-Pierre, N., Gardyna, S., Ginde, S., Goyette, M., Carlan, M., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levlne, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Mathews, C., McZarthy, M., McEwan, P., McRernan, K., McPheters, R., Maldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., Royler, J., Peterson, K., Rise, C., Rogov, P., Roman, J., Rosetti, M., Rise, C., Rogov, P., Roman, J., Rosetti, M., Rise, C., Schupback, R., Seamen, S., Schupback, R., Stalley, R., Schauer, S., Schupback, R., Stojanovic, N., Stojanovic, N., Stojanovic, N., Stojanovic, N., Stojanovic, N., Trayers, M., Trayers,
                                                                                                                                                                                                                                                                                                                            AC087828 186406 bp DNA linear HTG 07-APR-2001
Homo sapiens chromosome 15 clone RP11-292P13 map 15, WORKING DRAFT
SEQUENCE, 29 unordered pieces.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                    Gaps
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Insert size: 183606; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; agarose-fp
Quality coverage: 5.0 in Q20 bases; sum-of-contigs
      Length 174711;
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 15, clone RP11-292P13
                                                                    ö
Query Match 9.8%; Score 20; DB 9; Best Local Similarity 100.0%; Pred. No. 2.8; Matches 20; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC087828.2 GI:13560414
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                  COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens chromosome 11, clone RP11-4B7, complete sequence. AC026639 GI:16506908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                          Length 172915,
                                                                          300 others
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-4B7
                                                                                                                                                                               9.8%; Score 20; DB 2;
                                                                                                                                                                                                      Pred. No. 2.8;
Mismatches
          vector_side:right"
                                                                                                                                                                            9.5.,
100.0%; Pre-
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                                                                                                                                                                                                                                                                              94 cgaaagctaaaacgaattaa 113
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                                                                                                                                                                                                                             20; Conservative
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                                                                          52509 a
                         misc_feature
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ACCESSION
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AC026639/c
LOCUS
                                                                        BASE COUNT
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ORGANISM
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TITLE
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REFERENCE
AUTHORS
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Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Taelaye, Theddore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Vo, A., Wilson, B., Wix, Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

L. Direct Submission

L. Submitted (06-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
on oct 28, 2001 this sequence version replaced gi:15148319.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                         ..... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
------------- Project Information
Center project name: L8334
Center clone name: 4_B_7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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complement(10842. 11798)
/rpt_family="L1Mca"
11799. 1276.
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7042. .7192
/rpt_family="FRAM"
complement(7295. .7582)
/rpt_family="AluSc"
complement(8006. .9070)
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/rpt_family="LIMCa"
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complement(12753. .13028)
/rpt_family="AluJo"
complement(13029. .13089)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .4984
/rpt_family="L1PB2"
complement(5035. .5065)
/rpt_family="U2"
5055. .5060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="HAL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="LiME"
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complement(5680. .5796)
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complement(5374. .5650
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לרpt_family="AT_rich"
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5859, .5890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="Aluy"
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Cercopithedrinae; Papio.

1 (bases 1 to 172915)

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Dietrich, N.L., Todo, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q.,

Legaspi, R., Maduro, Q.L., Maduro, V.B., Mastello, C., Mastrian, S.D.,

McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y.,

Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Zhang, L.-H. and Green, E.D.

NISC Comparative Sequencing Initiative
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-NOV-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 171910 bases at least Q40
Consensus quality: 171910 bases at least Q30
Consensus quality: 17236 bases at least Q20
Insert size: 130000, agarose-fp
Insert size: 172615; sum-of-contigs
Quality coverage: 12.58x in Q20 bases; agarose-fp
Quality coverage: 9.47x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 2438: contig of 2438 bp in length
439 2538: gap of unknown length
1539 8133: contig of 5595 bp in length
1534 40378: contig of 13145 bp in length
1534 40478: gap of unknown length
172915: contig of 132437 bp in length
160cation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Papio cynocephalus anubis"
/db_xref="taxon:9555"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@hhgri.nih.gov
------- project Information
Center project name: ccy
Center clone name: 167P22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment" 8234. .40378 /note="assembly_fragment clone_end:T7
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             HTG; HTGS_PHASE1; HTGS_DRAFT.
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2539. .8133
                                 olive baboon.
Papio cynocephalus anubis
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Green, E.D.
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4077. 14120
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/rpt_family="AT_rich"
12263, 1261^
                                                                 /rpt_family="Alu"
11694. .11729
/rpt_family="A-rich"
11712. .11972
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18031. .18465
/rpt_family="(TA)n"
18455. .18515
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/rpt_family="ERVL"
18516. .1867
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/rpt_family="Alu"
/6014..160*
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/rpt_family="Alu"
16320 .164*
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/rpt_family="MIR"
14576. .14863
/rpt_family="Alu"
/rpt_family="Alu"
15648. .15823
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16015. .16319
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2232. .12264
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7256. .17384
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7639. .18045
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18643. .18952
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18923. .18952
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2908. .13739
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2235. .12261
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rpt_family="L1"
2611. .12907
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1973. .12231
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3743. .13876
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3885. .13934
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DEFINITION ACCESSION

VERSION

RESULT AC099742

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Submitted (30-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA on Jan 4, 2002 this sequence version replaced gi:13786481.
                                            PRI 30-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (07-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 154037)
Sulston,J.E. and Waterston,R.
                                        AC072054 154037 bp DNA linear PRI 30-J
Homo sapiens BAC clone RP11-33P21 from 7, complete sequence.
                                                                                                                                                                                                                                                                                                                              Coases 1 to 154037)
Edwards, J., Du, H., Haakenson, W. and Spalding, L.
The sequence of Homo sapiens BAC clone RP11-33P21
Unpublished (2001)
3 (bases 1 to 154037)
Waterston, R.H.
                                                                                                                                                                                                                                                                      Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                      AC072054.10 GI:18056706
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Waterston, R.H.
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                                                                                                                                            SOURCE
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu

code: WUGSC

Center project name: H_NH0033P21

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIRGTB/GTB/GRI/GRI sendemallto:egreen@nhgri.nih.gov/DIRGTB/GTB/GRI/GRI sendemallto:egreen@nhgri.nih.gov/or see http://genome.wustl.edu/gsc

SOURCE INFORMATION: The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,

/rpt_family="L1"

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP13-552B11; the clone sequenced to the left is RP13-552B11; the clone sequenced to the right is RP11-32P3, 2000 bp overlap. Actual start of this clone is at base position 22189 of RP13-552B11; actual end is at base position 2000 of RP11-32P3. Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) /organism="Homo sapiens" /db_xref="taxon:9606" rpt_family="AT_rich" /rpt_family="Alu" 8755. .8806 /rpt_family="(GGGA)n" 9513. .9762 /rpt_family="AT_rich" 10872. .10897 /clone="RP11-33P21" /clone_lib="RPCI-11" rpt_family="T-rich" Location/Qualifiers 789. .1317 /rpt_family="ERVL" 4289. .4432 rpt_family="(A)n" /rpt_family="(A)n" 10898. .11020 rpt_family="MaLR" /rpt_family="MIR" 4964. .5214 /rpt_family="Alu" 5994. .6283 /rpt_family="Alu" <461 6337. .6661 /rpt_family="Alu" 6636. .6661 /rpt_family="Alu" 10278. 1057 401. .7634 rpt_family="Alu" rpt_family="Alu" rpt_family="Alu" rpt_family="Alu" rpt_family="Alu" /rpt_family="L1" 5500. .5520 6991. .7114 /rpt_family="L1" 7354. .7433 797. .7843 'rpt_family="L1" l. .550 /rpt_family="L1" rpt_family="L2" 1y="L1" /chromosome="7" 10897 .10897 7634 8458 .9936 /rpt_famil 10577. 100 1. .154037 /map="7' 964 repeat_region source FEATURES

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Submitted (1947-1902) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasKer: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker. Center: Whitehead Institute/ MIT Center for Genome Research
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zenbek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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Location/Qualifiers
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1. .46765
/note="assembly_fragment
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Web site: http://www-seq.wi.mit.edu
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/map="15"
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Spaces 1 to 187676)

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Spaces 2 Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,Y., Boquslavki,L., Soukhagalter,B., Brown,A., Camarata,J., Campoplano,A., Chang,J.,. Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Choepel,Y., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Landers,T., Lehoczky,J., Levine,R., Liu,G., MacLean,C., MacLean,C., MacCan,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McCama,P., Major,J., Marquis,N., Matthews,C., Micol,R., Norbu,C., McCama,C., Wollon,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Reetla,R., Rieback,M., Raley,R., Rise,C., Rogdv,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schupback,R., Schupback,R
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Homo sapiens chromosome 15 clone RP11-692C24 map 15, WORKING DRAFT
SEQUENCE, 2 ordered pieces.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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gap of 100 bp
2: contig of 734 bp in length
100 bp
7: contig of 735 bp in length
gap of 100 bp
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2: contig of 705 bp in length
gap of 100 bp
9: contig of 726 bp in length
3: contig of 735 bp in length
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54541: contig of 737 bp in length
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55334: contig of 693 bp in length
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone RP11-692C24 Unpublished
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AC107958.2 GI:18653708
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
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43055: contig of 697 bp in length
43155: gap of 100 bp
43878: contig of 723 bp in length
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               McCarthy, M. McEwan, P., McKeynan, K., McPheeters, R., Meldrin, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Santos, R., Schupback, R., Schupaca, Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Trophan, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Vola, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Lobmitted (Ol-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 9, 2002 this sequence version replaced gi:17223322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
  Matthews, C.,
                                                                                                                                                                                                                                                                                                                                                                                           All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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------- Project Information
Center project name: L22005
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MacLean, C., Macdonald, P., Major, J., Marquis, N.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Olivier,M. and Cox, D.R.
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This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                1 13922: contig of 13922 bp in length 1923 36248: contig of 22226 bp in length 249 36348: gap of unknown length 249 36348: gap of unknown length 259 5226 bp in length 259 3226: gap of unknown length 259 32268: gap of unknown length 259 32268: gap of unknown length 259 122036: contig of 25876 bp in length 259 122036: contig of 29768 bp in length 259 122036: contig of 29768 bp in length 259 122036: contig of 40792 bp,in length 250 2588: gap of unknown length 250 2588: gap of unknown length 250 2588: contig of 40792 bp,in length.
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Stanford University School of Medicine
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
721: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: TTGTGGCCAAAGAAATCTCCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            504 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished, Olivier, M., Cox, D.R. (2000)
                                                                                                                                                                                                                                                         1. 162928
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-120K11"
/clone=lib="RP43"
1. 13922
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Michael Olivier, David R. Cox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vector_side:right"
29878 c 30533 g 50485 t
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                                                                                                                                                                                                                                                                                                                                                                                                                    14023. .36248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 36349. .66192
/note="assembly_fragment"
66293. .92168
/note="assembly_fragment"
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/note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                              vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                     clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0
Matches 30; Conservative
                   as soon as i
be preserved
                                                                                  14023
36249
36349
66193
66293
92169
122037
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                                                                      13923
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                                                                                                                                                                                                                                                                  source
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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JOURNAL
COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                               FEATURES
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G60919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
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nclu4034 61850 bp DNA linear HTG 09-FEB-2002
Homo sapiens chromosome 15 clone RP11-627K17 map 15, LOW-PASS
SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 61850)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone RP11-627K17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 61850)
2 (bases 1 to 61850)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B.
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, E., Morton, L., Hulme, W., Illev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAC ends sequenced at TIGR from the RPCIII BAC library. Designed and developed at the Stanford Human Genome Center.

Location/Qualifiers

/ Corganism="Homo sapiens"
/ Ab_xref="taxon:9606"
/ map="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                    : 95 degrees C for 10 minutes
94 degrees C for 30 seconds
60 degrees C for 30 seconds
72 degrees C for 23 seconds
30
Perkin Elmer 9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.3%; Score 21; DB 11; Length 579; 100.0%; Pred. No. 1.6; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                         25 ng
each 1 uM
each 200 uM
0.07 units/ul
5 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                      Amplifaq Gold Polymerase:
Total Vol:
Primer B: TCGCTTCTTTCTCCCTCCTAACT
STS_size: 327
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                             2.5 mM
50 mM
10 mM
8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 g
                                                                         Initial incubation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Human"
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                                                                                                                                           Polymerization:
PCR Cycles:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC104034.2 GI:18642791
HTG; HTGS_PHASE0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 TTTGTTCTTGCTCGTGTTTTG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 tttgttcttgctcgtgttttg 43
                                                                                                Denaturation:
Annealing:
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.51156)

repeat_region

(NID:91313113)	(NID:91313105)	(NID:91203721)	(NID:91312680)	(NID:91203720)	(NID:91312688)	(NID:9761262)	(NID:9761150)	(NID:91240743)	(NID:91202341)																						
W32120	W32085	N59831	W31561	N59830	W31628	EST R09339	R09227	N78042) EST N58451												•										
human EST	human EST	.28143) human EST	.28143) human EST	.28143) human EST	.28144) human EST W31628	human EST	.29853) human EST	human EST	.3135(human			.34778)		.37740)			.41706)	.41933)		.42982)	.44423)			.45669)	.45963)	.46597)			.50216)	.50791)	.50985)
/note="similar to	2768627838 /note="similar to	complement(27733. /note="similar to	complement(27838. /note="similar to	• 0	7. to	zb97c08.s1" 2866628972 /note="similar to	to.	14 lar to	yv71e06.r1" complement(31170. /note-"similar to	yv71e06.s1" 3197032006	/rpt_ramily="Li" 3226332563	/rpt_ramily="ALU" complement(34737.	/IPC_IAMIIY_LI 36558. 36709 /rpt_familv~"ALU"	complement (37630.	3983940125	/IPC_ISMILY - ALO 4012640157 /rpt family="I.1"	complement(41340.	/rpt_ramily="ALU" complement(41904.	/IPC_Idmily	complement(42942.	/rpt_ramlly="L1" complement(44380.	4465944954	/rpt_ramlly="ALU" 4542245448	/rpt_tamily="L1" complement(45615.	/rpt_ramily="L1" complement(45672.	complement (45964.	/rpt_ramily="Li" 4610046516	/rpt_family="L1" 4837048785	/rpt_tamily="L1" complement(49577.	/rpt_tamily="L1" complement(50540.	/rpt_ramily="The" complement(50820. /rpt_family="THE"
	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region

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AC104475 162928 bp DNA linear HTG 12-DEC-2001
Pan troglodytes clone RP43-120K11, WORKING DRAFT SEQUENCE, 6
unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 16298)
Akhter N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Legaspi, R., Maduro, C.L., Maduro, V.B., Masiello, C., Masirian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhangi, L. H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (12-DEC-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 161001 bases at least Q40 Consensus quality: 161422 bases at least Q20 Insert size: 143000; agarose-fp Insert size: 163428; sum-of-contys Quality coverage: 10.76% in Q20 bases; agarose-fp Quality coverage: 9.47% in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                           Length 156214;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                        Query Match 14.7%; Score 30; DB 9; Le Best Local Similarity 100.0%; Pred. No. 9.5e-06; Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                         /rpt_family="L1"
complement(51765. .52058)
/rpt_family="ALU"
complement(52252. .52467)
                                                                                                        .51764)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: ces
Center clone name: 120K11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE1; HTGS_DRAFT.
complement(51124. ... /rpt_family="L1" 51405. .51691 /rpt_family="ALU" complement(51721. ...
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2 (bases 1 to 162928)
Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: NISC
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Pan troglodytes
                                                      repeat_region
                                                                                                        repeat_region
                                                                                                                                                          repeat_region
                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
AC104475/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
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library contains cloned DNA from a human male fibroblast cell line 978SK. For references see: Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996).
                                                                                                                                                   NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of H_RG016J04;
actual end is at 156214 of H_RG016J04. The orientation of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to human EST AA123941 (NID:g1682616)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27125. .27544
/note="similar to human EST AA151796 (NID:g1720491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to human EST AA151807 (NID:g1720502)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA149579 (NID:91720380)
                                                                                                                                                                                                                                                                     This clone contains STS sWSS2784 (NID:g1113580) and sWSS893 (NID:g454733).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(27441. .27890)
/note="similar to human EST N52554 (NID:g1193720)
yvy36allar
27686. .27856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to human EST T02878 (NID:9314119)"
19436. 19497
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/rpt_family="ALU"
/rpt_family="L1"
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complement(9406. .9975)
/rpt_family="L1"
complement(10000. .11285)
/rpt_family="L1"
/rpt_family="L1"
/rpt_family="L1"
11666. .11687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(25561. .25578)
/rpt_family="L1"
complement(26832. .27124)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="CITB-978SK-B"
15. .40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .11285)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(25113. .25148)
                                                                                                                                                                                                                                                                                                                                                  1. .156214
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326. .621
/rpt_family="ALU"
complement(977. .1499)
/rpt_family="L1"
3398. .3421
                                                                                                                                                                                                                                                                                                              733).
Location/Qualifiers
                                                                                                       Selection: chloramphenicol
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27125. .27383
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="7q21"
/clone="RG016J04"
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5319. 531
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/rpt_family="L1"
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27125. .275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            z139c02.s1"
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                                                                                                                                                                                                                              clone is unknown.
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BLHHLLGWKILLIDVSNNMRINOYPESNAPIALSEPDSLIVKGRNVYSAMALQLEPKD
ASROYYICSNNIQAROVIELENGINFIDLGSLSSAREIRUFD-ELFLERFETURGPVV
AISLATFFFLYSFVRDVIHPYARNQOSDFYKIPIEIVNRTLPIVAITLLSLVYLAGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send an E-mail to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRI 09-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 155214)
Gattung, S. and Maggi,L.
The sequence of H. sapiens BAC clone RG016J04
Onpublished (1997)
2 (bases I to 155214)
Waterston,R.
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Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, MO 63108, USA
http://genome.wustl.edu/gsc
e-mail: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; L
1.6e-05;
     'note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                                                                        14.7%; Score 30; DB 100.0%; Pred. No. 1.6:ive 0; Mismatches
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Best Local Similarity 100.
Matches 30; Conservative
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DEFINITION ACCESSION

RESULT 2 HSAC002064

В õ

SOURCE

VERSION KEYWORDS

AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

BASE COUNT ORIGIN

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AC026639 Homo sapi
AC081245 Homo sapi
AC01245 Homo sapi
AC026813 Waus muscu
AC026813 Waus muscu
G57411 SHGC-103088
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AP000199 Homo sapi
Continuation (19 o
AP000239 Homo sapi
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2453)
Afar,D.E., Hubert,R.S., Raitano,A.B., Saffran,D.C., Mitchell,S.C., Faris,M. and Jakobovits,A.
Serpentine transmembrane antigens expressed in human prostate cancers and uses thereof Patent: WO 0140276A 7 07-JUN-2001;
Urogenesys, Inc. (US)
Urogenesys, Inc. (US)
                                              AC104034 Homo sapi
AC107958 Homo sapi
AC072054 Homo sapi
AC099742 Papio cyn
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AL003022 Streptomy
AL022374 Streptomy
AC05222 Homo sapi
AC102850 Mus muscu
AC003670 Homo sapi
AL138659 Arabidops
AL356014 Arabidops
AC108704 Homo sapi
AC108704 Homo sapi
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AC108704
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14.7 156214
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                                                                                                                                                                                                                                                           3595312
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                             residues
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                                                                                September 20, 2002, 09:55:54
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    nucleic search, using sw model

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                                                                                                                    Nelson, P.S., NW.-L., Schummer, M., True, L.D., Liu, A.L., Bumgarner, R., Ferguson, C., Dimak, A. and Hood, L.
and sxpressed-sequence-tag database of the human prostate: sequence analysis of 1168 cDNA clones
Genomics 47 (1), 12-25 (1998)
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                  Contact: Nelson PS

Contact: Nelson PS

Department of Molecular Biotechnology
University of Washington
Box 357730, HSB K380, 1705 NE Pacific, Seattle, WA 98195, USA
Tel: 206 685 7336
Fax: 206 685 7301
Email: psnels@u.washington.edu
Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21; DB 9; Length 618;
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AV731102.1 GI:10840523
 AA447322
AA447322.1 GI:3025408
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/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
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                                                                                                                                                                                                                                                             Length 645;
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            This clone is available at CHGC in Shanghai.
Location/Qualiflers
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Pred. No. 4.6;
0; Mismatches
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/lab_host="SOLR"
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Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
Email: hanzg@chgc.sh.cn
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PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clonelDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares NbHSF pool 1: 145032-147335, 147720-148103, 148872-149255, 15002-150407, 151176-152327 Soares NbHRF-9W pool 1: 358280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 326280-32663 Soares NbHOP pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 518)
Salanoubat, M., Choisne, N., Artiquenave, F., Brottier, P., Wincker, P., Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSOOQB1 518 bp DNA linear GSS 28-JUN-1999 Arabidopsis thaliana genome survey sequence SP6 end of BAC FllA13 of IGF library from strain Columbia of Arabidopsis thaliana,
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Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Location/Qualifiers
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SA.CO8R PN001-Normal Human Prostate Homo sapiens cDNA clone SA.CO8
5', mRNA sequence.
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100.0%; Pred. No. 4.5;
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/organism="Arabidopsis thaliana"
/strain="Columbia"
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/clone_lib="IGF"
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                                                                   /organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:255116"
/clone="IMAGE:255116"
/clone="IMAGE:255116"
/clone="IMAGE:255116"
/clone=lib-"Scares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
//note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site=1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares Nb2HF pool 1:
145032-147335, 147720-148013, 1448872-14555, 15002 -
150407, 151176-15237 Soares Nb2HF8-9W pool 1:
145032-147335, 7720-148013, 148872-145653 Soares NbHOT pool 1: 723720-72607, 733080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 512)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs:r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 468.
Location/Qualifiers
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mab65f07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:3272605 3', mRNA sequence.
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Pred. No. 4.5;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3272605"
       High quality sequence stop: 461.
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Best Local Similarity 100.0%
Matches 21; Conservative
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Unpublished (1997)
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//dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: colon; Vector: pucl8; Site_1: Smal; Site_2:
//mote="Organ: colon; Vector: pucl8; Site_1: Smal; Site_2:
//mote_mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
//16 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                            1 (bases 1 to 450)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., Geoliveire, P.S., Bucher, P., Jongeneel, C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QVO-CT0225-230 300-169-g06&t3=2000-03-23&t4=1) seq primer: puc 18 forward High quality sequence start: 3 High quality sequence start: 3 High quality sequence stop: 450.
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                                                                          AW852181 450 bp mRNA linear EST 19-MAY-200 QVO-CT0225-230300-169-906 CT0225 Homo sapiens CDNA, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
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/db_xref="taxon:9606"
/clone_lib="CT0225"
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+55-11-2707001
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REFERENCE | Enhancistic Metazon Chordata; Vertebrata; Enteleostomi; REFERENCE | Tobases 1 Codes | Code
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us-09-802-520-7.rst

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Matches 21; Conservative
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Best Local Similarity 100.
Matches 21; Conservative
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BF372093/c
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/db_xref="taxon:9606"
/clone="InhGE:909830"
/clone=lib="NcI_CGAP_EW1"
/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
/note="Vector: pAMP10; mRNA made from Ewing's sarcoma,
/note="Vector: pamp10; manual pamp10;
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//dev.strage="Adult"
//dev.strage="Adult"
//note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES POCR (U.S. Letters Patent application No. 196
//16 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 407)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
Simpson,A.J.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=£t2=QVO-CT0225-230 300-169-b05£t3=2000-03-23£t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence start: 12
High quality sequence stop: 407.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Pred. No. 4.1;
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/db_xref="taxon:9606"
/clone_lib="CT0225"
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100.0%; Pre
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/note="Organ: prostate_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A min!-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under to 75 c 64 g 150 t
                                                                                                                                                                                                                                                                                      pr3/2U93 407 bp mRNA linear EST 24-NOV-2000 QV2-FT0010-090800-303-g05 FT0010 Homo sapiens CDNA, mRNA sequence. BF372093
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: sainpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-FT0010-
090800-303-905&t3=2000-08-09&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 407.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Liaboratory of Cancer Genetics
Liudwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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100.0%; Pred. No. 4.4
ive 0; Mismatches
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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Loudiscope.

Submission

2 rue Gaston Cremieux, CP 5706, 91057 EVRV cedex, FRANCE. (E-mail: Seqref@genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces hansenii, Rluyveromyces inethis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 248)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Sllva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M. Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                  Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S.,
Belotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S.,
Belotin-Fukuhara, M., Dujon, B., Durrens, P., Lephingle, A., Liborente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Whorker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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/strain="CBS 712"
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100.0%; Pred. No. 1.5;
iive 0; Mismatches 0
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Mismatches
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/db_xref="taxon:4911"
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/clone_lib="XAZ0AA"
/note="end : T7"
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                         (bases 1 to 978)
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283 bp mRNA linear EST 19-AUG-1997 sequence.
AA491988.1 GI:2221550
EST 19-AUG-1997
AA491988.1 GI:2221550
EST
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//dev_stage="Adult"
//note="Organ: ovary; Vector: puc18; Site_1: Smal; Site_2:
Smal; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
//16 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 880 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 276.
Location/Qualifiers
                                                                                                                                                                            Figure 1. Saimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-OT0067-060700-277-f06&t3=2000-07-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 248.
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Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Natlonal Cancer Institute, Cancer Genome Anatomy Project (GGAP),
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Pred. No. 4.1;
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/organism="Homo sapiens"
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/clone_llb="OT0067"
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1Duo16F03 Bos taurus Duodenum #1 library Bos taurus cDNA, mRNA
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(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatina Bonaldo. 116 t
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene Expression Profiling of the Bovine Gastrointestinal Tract Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
All Agriffor, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada Tel: 780 492 0169
Fex: 780 492 4265
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/db_xref="taxon:9913"
/clone_lib="Bos taurus Duodenum #1 library"
/tclone_lib="Bos taurus Duodenum #1 library"
/tcll_type="Simple columnar epithelial"
/dev_stage="Young adult"
/deb_host="Xoung adult"
/note="Young adult"
/not
                                                                                                                                                                                                                                                                                                                                                                                                                                              181 ctgaataaaactgaattctctccagtttaaagcattgctcactgaagggatagaagtgac 240
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                                                                                                                                                                                                                                                                                      Length 393;
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Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E.,
,P.M.K. and Moore,S.S.
                                                                                                                                                                                                                                                                                   Query Match 32.1%; Score 85; DB 9; L. Best Local Similarity 100.0%; Pred. No. 5.1e-33; Matches 85; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 4.2e-19;
Live 0; Mismatches 0;
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Insert Length: 558 Std Error: 0.00
POLYA=No.
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/organism≈"Bos taurus"
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
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199

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Single pass sequencing. Bases called and alt_trimmed with phred v0.9809044.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNSU/1AX 978 bp DNA linear GSS 06-JUL-2001
T7 end of clone XAZ0AA001H01 of library XAZ0AA from strain CBS 712
of Kluyveromyces marxianus, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
EST 01-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
I (bases 1 to 978)
Llorente, B., Malpertuy, A., Blandin, G., Artiguenave, F., Wincker, P. and Dujon, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 595;
  BI359597 595 bp mRNA linear 384188 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.3%; Score 30; DB 10; Length 59
100.0%; Pred. No. 0.00011;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kluyveromyces marxianus var. marxianus
FEBS Lett. 487 (1), 71-75 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 gtgactgccaggagggaaagtaagccaagg 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Sus scrofa"
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/clone_lib="MARC_2PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 132 row: H column: 3
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kluyveromyces marxianus.
Kluyveromyces marxianus
                                                           BI359597.1 GI:15055625
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GSS.
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Best Local Similarity 100.
Matches 30; Conservative
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AUTHORS
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R26307 yh49a03 r1 BF661645 maa64b03 BF452991 maa64b03

AV273266

BB048145

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnh.gov/bbrp/image/image.html
Insert Length: 305 Std Error: 0.00
Seq primer: -40ml3 #wd. EF from Amersham.
Location/Qualifiers
                                                                                      BB213248 BB213248
AV222888 AV232888
BB687167 uv99g10.x
AV027007 AV027007
BH53900 RPCI-24-9
         BB479717 BB479717
AW011108 ST16G11 P
AQ833520 HS_5304_B
BG403540 602419242
                                                                                                                                                                                                                                                                                                                                                                                               AIO16724 393 bp mRNA linear EST 27-AUG-1998 ov03d03.xl NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636229 3',
                                                                                                                                                                                                               AV353049 AV353049
AV016593 AV016593
BB059246 BB059246
AV314454 AV314454
BB296861 BB296861
AV013960 AV013960
AV026902 AV0289977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. L (bases 1 to 393)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                          AV273266 BB056822 BB296994 BB048145 BAV021787 AV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/clone="IMAGE:1636229"
/clone=1ib="NOI_CGAP_Kid3"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                   AV232888
BE687167
                                                                                                                                               вн053900
                                                                                                                         AV020448
AV027007
                                                                                                                                                            AV273266
BB056822
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BB048145
AV021787
AV353049
AV016593
BB059246
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BB296861
AV013960
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                                                                                         BB213248
                                                                                                                                                                                                                                                                                   AV026902
                                                                                                                                                                                                                                                                                                                                                                                                                                           AI016724.1 GI:3231060
                                                      Tumor Gene Index
Unpublished (1997)
mRNA sequence.
AI016724
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RESULT 1
AI016724
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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 B1559597 384188 MA
AL424687 T7 end of
BF360898 NOV-07006
AA401988 NE72609 QV2 FT001
BF372093 QV2 FT001
BF372093 QV2 FT001
BF14610 7j65c01.x
AW044547 wy83a03.x
BF14459596 nab65f07.
AL085579 Arabidops
AA447322 SA.COBR P
AV731102 AV731102
AW7311549 AV731162
AW771549 BF384148
                                                                                         (without alignments)
707.777 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI016724 ov03d03.x
BM431438 1Duo16F03
                                                                           September 20, 2002, 08:33:51; Search time 5053.42 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                              1 ctcagtctgggtatctgcaa......ggagggaaagtaagccaagg 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                    27472414
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                       13736207 segs, 6748477542 residues
                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                           summaries
                                                      nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNSO71AX
BF360898
AA491988
AW852172
BF372093
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BF114610
AW044547
                                                                                                                                                                     OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                        length: 0
length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_gss:*
em_gss_hum:*
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em_esthum:*
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gb_htc:*
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Match Length
                                                                                                                                                                                                                                                                                                                               EST:*
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0

Word size :

Searched:

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Minimum DB seq Maximum DB seq

Database :

BE848896 uv99910.y

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors

CNS000B1 AA447322 BF439596

885 221 221 221 221 221 221 221 231

00000000

Score

Result . 9 AV731102 AV731549 AW971939

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Query Match
6.0%; Score 16; DB 2; Length 1443;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels

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0; Gaps

QQ

Search completed: September 20, 2002, 09:51:17 Job time: 11865 sec

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Gaps
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24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTRESSORTE ADDRESSEE: Folgy & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM: WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/403,853
FILING DATE: 30-MAY 1995
CLASSIFICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 24-SEP-1993
PRIOR APPLICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 25-SEP-1993
PRIOR APPLICATION NUMBER: AU PL 4973
FILING DATE: 25-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, SLEPHEN A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 20,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HODSON, Peter J.
APPLICANT: LAH, Maria
APPLICANT: LAH, Maria
APPLICANT: RORT, Alex A.
APPLICANT: RYNEL, John L.
APPLICANT: ATWELL, John L.
APPLICANT: MALBY, Robyn L.
APPLICANT: POWER, Barbara E.
APPLICANT: COLMAN, Peter M.
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
NUMBER OF SQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                       Query Match 6.0%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 24; Matches 16; Conservative 0; Mismatches
      EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SSOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/08403853 Patent No. 5844094 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 1443 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (202)672-5300
(202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 GGGAAGTAAGCCAAG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 gggaaagtaagccaag 264
                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-328-111-84
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18-09-328-111-84/C

18-09-328-11-84/C

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18-09-328-
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APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                   ZIP: 94304
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/541,228
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BAllings, Lucy J
REGISTRATION NUMBER: PF-0118 US
FELECOMONICATION INFORMATION:
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2161 base pairs
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.4%; Sor
Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
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LIBRARY:
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                                                                                                                                                                                                                   CITY: Pal
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; CLONE: C
US-09-541-228-4
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                  Length 2161;
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                  6.4%; Score 17; DB 2;
100.0%; Pred. No. 7.4;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FASTEDQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111.444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
                                                                                                                                                                                        RESULT 12
US-09-111-444-4/c
; Sequence 4, Application US/09111444
; Patent No. 6045792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-541-228-4/c

Sequence 4, Application US/09541228
Patent No. 6232077
GENERAL INFORMATION:
APPLICANT: AP-1009, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
                                                                                                                    2027 AAGTACTTATGAGCAGA 2011
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                                                                                              144 aagtacttatgagcaga 160
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                                      Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-111-444-4
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                      Query Match
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APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: STATEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herwith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
RECISTRATION NUMBER: 36,749
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECHONE: 415-855-0555
ITELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2161 base pairs
                                      00786/327001
            REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786
TELECHONE: 617/542-5070
TELEX: 200154
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08712709
Patent No. 5863780
                                                                                                                                                                                                                                                                                      Coding Sequence 127...1404
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Fraser, Janis K.
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STRANDEDNESS: sing
                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LIBRARY:
; CLONE: Consensus
US-08-712-709-4
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US-08-712-709-4/C
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                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-09-185-370-1
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Fis
STREET: 225 FI
CITY: Boston
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US-09-185-370-1/c
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STATE: MA
COUNTRY:
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APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.42709
CURRENT FILING DATE: 1999-11-12
CURRENT FILING DATE: 1999-11-12
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 301;
.0.055;
ches 0; Indels
                                                                                                                         Query Match 7.9%; Score 21; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 0.054; Matches 21; Conservative 0; Mismatches 0; Indels
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APPLICANT: Force, John M.
APPLICANT: Fombo, Celia M.
APPLICANT: Bonventre, Joseph
TILE OF INVENTION: SOK-1 AND METHODS OF USE
NUMBER OF SEQUENCES: 10
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ADDRESSEE:
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                            Sequence 288, Application US/09439313 Patent No. 6329505
                                                                                                                                                                                                                                                                                                                                                                                                                   Harlocker, Susan Louise
Jiang Yuqui
Reed, Steven G.
Kalos, Michael
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Sequence 1, Application US/08852743

; Patent No. 5830699

; GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Best Local Similarity 100.(
Matches 21; Conservative
                                 TYPE: DNA
ORGANISM: Homo Sapiens
US-09-323-873A-10
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CORGANISM: Homo sapien
US-09-439-313-288
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ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                 US-09-439-313-288
     SEQ ID NO 10
LENGTH: 180
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LENGTH: 301
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APPLICANT:
APPLICANT:
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APPLICANT:
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Patent No. 6093560
GENERAL INFORMATION:
APPLICANT: FORCE, Thomas
APPLICANT: Pombo, Celia M.
APPLICANT: Bonventre, Joseph
TITLE OF INVENTION: SOR-1 AND METHODS OF USE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,743
FILING DATE: 7-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION UNMBER: 60/016,774
FILING DATE: 7-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
OPERATING SYSTEM: Windows95
CUSTWARE: FastSED for Windows Version 2.0
CUSTRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/185,370
                                                                                                                                                                                                                                                                                  00786/327001
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                                                                                                                                                                                                                                  NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFRENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-6070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: Coding Sequence
; LOCATION: 127...1404
US-08-852-743-1
                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617/742-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1975 base pairs
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Best Local Similarity 100.
Matches 17; Conservative
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER:
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Gaps
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APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Bouglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF;
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: 05/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                               APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 366;
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4.5e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
      93 CTGCCAGGAGGGAAAGTAAGCCAAGG 118
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                                                                                                                                    Sequence 215, Application US/09439313 Patent No. 6329505
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; Sequence 10, Application US/09323873A
; Patent No. 6329503
                                                                                                                                                                                                                                                                       Harlocker, Susan Louise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)...(366)
; OTHER INFORMATION: n = A,T,C or
US-09-439-313-215
                                                                                                                                                                                                    APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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ORGANISM: Homo sapien
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 215
LENGTH: 366
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APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
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                                                                                                                                                                                                      Length 250;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCATION DATA:
CARRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
                                                                                                                                                                                                 DB 4; Le
9.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.5%; Score 86; DB 4; L6
100.0%; Pred. No. 4.5e-36;
tive 0; Mismatches 0;
                                                                                                                                                                                               35.1%; Score 93; DB 100.0%; Pred. No. 9.5 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEFHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 233 gaagtgactgccaggagggaaagtaagccaagg 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 ctgccaggagggaaagtaagccaagg 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 215, Application US/09030607 Patent No. 6262245
                                        FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(250)

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 93, Conservative
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TYPE: nucleic acid
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Best Local Similarity 100.
Matches 86; Conservative
TYPE: DNA
ORGANISM: Homo sapien
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US-09-030-607-215
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COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
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Patent No. 6329505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Hatcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.1'
Best Local Similarity 100.
Matches 93; Conservative
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                    CORRESPONDENCE ADDRESS:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: cDNA
US-09-030-607-213
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STREET: bocc
TTTY: Seattle
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US-09-439-313-213
                                                     ADDRESSEE:
                                                                                   CITY: Sec
STATE: WA
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                                                 367 GAAAGTACTTATGAGCAGAGGGACATATCCAAGTGTAGACTGAATAAAACTGAATTCTCT 308
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APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REPERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR FILING DATE: 1998-06-01
                                                                                                                        gaaagtacttatgagcagagcgacatatccaagtgtagactgaataaaactgaattctct
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6262245
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Patent No. 6329503
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
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APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 155; Conservative
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US-09-323-873A-7
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Best Local Similarity
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APPLICANT: Reed, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Fanger, Gary
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 250;
                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APLICATION DIAGNOSIS OF PROSTATE CANCER CURRENT APPLICATION NUMBER: 05/09/439,313

CURRENT APPLICATION NUMBER: 05/09/439,313

CURRENT FILLING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 575

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 213

LENGTH: 250
                                                                                                                                                                                                                                                                                                  FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 213:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.1%; Score 93; DB 100.0%; Pred. No. 9.5
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Issued_Patents_NA:*
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 /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
 /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
 /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
 /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
 /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
 /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*

Post-processing: Listing first 45 summaries

Database

Appli Sequence 3, Appli Sequence 7, Appli Description Sequence Sequence Sequence sedineuroe US-09-030-607-213 US-09-030-607-213 US-09-439-313-213 US-09-333-873-10 US-09-333-873-10 US-09-333-873-10 US-09-185-743-11 US-09-185-743-11 US-09-185-743-11 US-09-111-444-4 US-09-111-444-4 US-09-111-444-4 US-09-111-444-4 US-09-111-444-4 US-09-111-444-4 US-09-111-444-4 US-09-111-444-4 US-08-111-444-4 US-08-111-444-4 US-08-411-560-20 SUMMARIES DB Length 1213 521 250 250 366 366 180 1975 1975 2161 2161 25161 25161 25161 25161 25161 2517 25161 2517 Query Score õ 00000

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119, 1103, 1103, 1206, 1206, 112, 112, 112, 112,	Ø	Gaps
Sequence Seq	PROTÈ IN	3;
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74-19 	S C. C. S/MS-D	DB 3; .5e-1
43-81(0 23-91) 23-91) 23-91) 33-65/ 33-65/ 33-65/ 33-65/ 33-66-31 66-31	ALIGNMENTS GROWTH-ASSOCIATED MEMBRANE GROWTH-ASSOCIATED	re 244; ed. No. 6 Mismatche
US-08-643-810A-19 US-09-552-613-11 US-09-123-912-103 US-09-328-111-206 US-09-328-111-206 US-09-328-111-206 US-09-328-111-210 US-09-328-111-210 US-09-26-315-12 US-09-26-315-12 US-09-26-315-12 US-09-26-315-12 US-09-26-315-12 US-09-26-315-12 US-09-26-315-12 US-09-26-315-12 US-09-26-315-12 US-09-26-315-12 US-09-26-315-12 US-09-26-315-12 US-08-517-13A-8 US-08-517-12 US-08-517-12 US-08-517-12 US-08-517-12	ALIGNM 1	Scc Pr ,
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60 4 4 9 6 6 9 6 9 6 9 6 9 6 9 6 9 6 9 9 6 9 9 6 9 9 6 9 9 6 9 9 6 9 9 6 9 9 6 9	ication US/0) 70 TION: adj. Preeti adj. Preeti orley, Nail orrer PHAR INCYTE PHAR 74 PORTER DR ALTO IS ADDRESS: INCYTE PHAR INCYTE PHAR ALTO IS ELOPPY dii IBM PC COMpa VSTEN: PC-DR VSTEN: PC-DR IS ELOPPY dii IBM PC COMpa VSTEN: PC-DR IS INUMBER: US, INUMBER: US, INUMBER: 3 OCCET UNBER (650) 855-03 (650) 855-0	vat
C C C C C C C C C C	3,C Application U Application U ORMATION: Gual, Preet; Gualer, N INVENTION: COTICY, Ne INVENTION: DENCE ADDRESS BE: INCYTE P A174 PORTER PALO ALTO CALIFORNIA A174 PORTER PALO ALTO SYSTEM: TYPE: Floppy CC NG SYSTEM: NG PORTER READABLE FORW A200 PORTER A100 NUMBER: CCATION DATE: PECATION NUMBER: CERRON INFORMA AGENT INFORMA INFORMACTERITY INFORMA INFORMACTERITY INFORMA INFORMACTERITY INFORMACTERIT	92 Similarity 10 4; Conservativ
20020000000000000000000000000000000000	SULT 1 -09-083-521-3/C Sequence 3, Application US/090835 Patent No. 6048970 GENERAL INFORMATION: APPLICANT: Guegler, Karl J. APPLICANT: Corley, Neil C. TITLE OF INVENTION: PROSTATE NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: ADDRESSE: INCYTE PHARMACEU STARET: A114 PORTER DRIVE STREET: 3174 PORTER DRIVE STREET: A120 ALTO STARTE: CALIFORNIA COMPUTER: EADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-005/MS SOFTWARE: WORD PETFCT 6.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/0 FILING DATE: HELEWITH APPLICATION NUMBER: 39,132 REFERENCE/POCKET NUMBER: BF TELECOMMUNICATION INFORMATION: REGISTRATION NUMBER: 39,132 REFERENCE/POCKET NUMBER: BF TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 85-0555 TELECOMMUNICATION INFORMATION: TO ON	Simi 4;
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27-JAN-2000

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The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polymucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polymucleotides encoding them, antigen presenting cells which express the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polymucleotides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06641 to AAA06691 and AAA080000 to AAV82000 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                     New polypeptide useful for treating and diagnosing prostate cancer comprises an immunogenic portion of prostate tumor protein - \,
                                                                                                                                                                                                                                       Mitcham JL;
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                                                                                                                                                                                                                                       Xu J,
                                                                                                                                                                                                                                       Yuqiu J,
                                                                                                                                                                                                                                                                                                                                                     Claim 50; Page 173; 263pp; English.
                                                                               98US-0116134.
98US-0159812.
98US-0159822.
99US-0232149.
99US-0232880.
                                                                 98US-0115453
                                   99WO-US15838
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                                                                                                                                                                                                                                       Harlocker
                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                     WPI; 2000-171268/15.
                                                                               14-JUL-1998;
23-SEP-1998;
23-SEP-1998;
15-JAN-1999;
15-JAN-1999;
09-APR-1999;
                                 14-JUL-1999;
                                                                                                                                                                                                                                    Dillon DC,
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ö Gaps ; Query Match 35.1%; Score 93; DB 21; Length 250; Best Local Similarity 100.0%; Pred. No. 4.3e-37; Matches 93; Conservative 0; Mismatches 0; Indels qq ò

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Search completed: September 20, 2002, 09:59:56 Job time: 11714 sec

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AAV61347 RESULT

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This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a blological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 agtgtagactgaataaaactgaattctctccagtttaaagcattgctcactgaagggata 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; prostate cancer; diagnosis; tumour; gene therapy; detection; immunogenic; cytostatic; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                              Novel human prostate specific tumour protein and fragments - useful
                                                                  specific gene; human; prostate cancer; detection;
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                                 specific gene clone 8-b5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 130; 141pp; English
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08-DEC-1998 (first entry)
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                                 Prostate tumour
                                                                  Prostate tumour
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01-AUG-1997;
                                                                                                                   Homo sapiens
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                                                                                   therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.
                1502 TGTAGTACTCTTCCTCAAAAGCTCGTTTCCATCCATAAATTAAAAACATGGAAAGTACTTA 1443
tgtagtactcttcctcaaaagctcgtttccatccataaattaaaacatggaaagtactta 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 agtgtagactgaataaaactgaattctctccagtttaaagcattgctcactgaagggata 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                             Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
                                                                                                                                                                                                                                                                             Reverse DNA sequence of prostate tumour clone 8-b5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 250 BP; 81 A; 53 C; 42 G; 69 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 93; DB 19;
Pred. No. 4.3e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.1%; Scc. 100.0%; Pred. No. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 tgagcagagcgacatatccaagtgtaga 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 121; 130pp; English
                                                                                                                                                                                BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                              AAV61347 standard; cDNA; 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US03492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97us-0806099,
97us-0904804.
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                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
nes 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-609886/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon DC, Xu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides
                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                            WO9837093-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-1998:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1997;
                                                                                                                                                                                                                                             06-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-1997
                                                                                                                                                                                                             AAV61347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
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RESULT 14

AAV58683 ID AAV5 XX AC AAV5 XX

233

86

Matches

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Gaps

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Length 250;

us-09-802-520-7.rng

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liver cancer; lung cancer; cytostatic; ds.
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                                                                                                                                                                                                                                                                            The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer;
benign prostatic hyperplasia; acute prostatitis; testicular cancer;
cryptorchidism; testicular disorder; proliferative disorder; lymphoma;
leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
                                                                                                                                                                                                New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                    рę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgtagtactcttcctcaaaagctcgtttccatccataaattaaaacatggaaagtactta 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 CCAGAATTACAATTGAGGCCAAAACAAGAGCAAGAACAAAGTTTGGTGGTGTATAAAATC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 TGTAGTACTCTTCCTCAAAAGCTCGTTTCCATAAAATTAAAAACATGGAAAGTACTTA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 ccagaattacaattgagggcaaaacaagagcaagaacaaagtttggtgtgtataaaatc 92
                                                                                                                                                                                                                                                                                                                                                                                                     prostatic hyperplasia, acute prostatitis, testicular cancer, cryptocolididism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, liver cancer and lung cancer. The present sequence represents exon 6 of a prostate specific protein, six-Transmembrane Protein of Prostate 1, STMPL, alternatively
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 148 BP; 36 A; 29 C; 26 G; 57 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 55.8%; Score 148; DB 22; Best Local Similarity 100.0%; Pred. No. 8.9e-65; Matches 148; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 tgagcagagcgacatatccaagtgtaga 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Fig 4F; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS15793 standard; DNA; 1725 BP
                                                                23-MAR-2001; 2001WO-US09410
                                                                                           24-MAR-2000; 2000US-191929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spliced version, ORF2.
                                                                                                                      (SAAT/) SAATCIOGLU F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                         WPI; 2001-662926/76.
           WO200172962-A2.
                                                                                                                                                Saatcioglu F;
                                       04-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS15793;
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testis-specific polypeptides and the nucleic acids encoding them.
Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign of the testis or prostate prostatifis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence encodes a prostate specific protein, Six-Transmembrane protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                   **tag= b
/note= "Represents 12713 nucleotides of intron 2"
                                                                                                                                                                                                                                                                                                                                                   d
"Represents 1396 nucleotides of intron 3"
                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= e
/ote= "Represents 2372 nucleotides of intron 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= f
/note= "Represents 2299 nucleotides of intron 5"
                                                                                                            *tag= a
'note= "Represents 338 nucleotides of intron 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 4B; 114pp; English.
                                                                                                                                                                                                                                                                                               'product= "STMP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US09410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAR-2000; 2000US-191929P.
                                                                                                                                                                                                                                         200..1702
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Best Local Similarity 100.0
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                   /*tag=
/note=
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Homo sapiens
                                                                            misc_feature
                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                            misc_feature
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us-09-802-520-7.rng

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Predicted transmemorate domains, but is encoded by a distinct gene, clocalised transmemorate domains, but which show no significant structural conservation, but which show no significant structural conservation, but which show no significant structural common proteins. STRAP-1 is characterised by six caracterised by six transmembrane domains and intracellular N- and C-termini, suggesting tracellular loops. STRAP-2 exhibits a manner into three extracellular and two intracellular loops. STRAP-2 exhibits a manner into three extracellular and two intracellular loops. STRAP-2 exhibits a markedly different mRNA and protein expression profile relative to STRAP-1, suggesting that these conversation appears to be very prostate specific, as significant mRNA expression is not detected in a variety of normal tissues. STRAP-2 expression is downrequiated in some prostate cancers, whereas STRAP-1 expression is generally absent. The function of the STRAP proteins is not cancers, may be ion channels (from the presence of six transmembrane domains, a feature which is shared by certain ion channels) or gap-junction proteins (from immunohistochemical staining). STRAP-1 and STRAP-expressing cells. STRAP proteins may be used to identify specific-binding agents, to produce anticancer vaccines and to generate specific-binding agents, to produce anticancer vaccines and to generate specific antibodies. The antibodies may be used for detection, prognosis, and monitoring of cancers (or susceptibility to cancer), as therapeutic and muchical action or target therapeutic agents to their site of action. STRAP muchical action and the stail and stail and the stail and the stail and the stail and the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic and prognostic reagents, for identifying STRAP-expressing cells for screening inhibitors of STRAP expression and for therapeutic modulation/inhibition of STRAP expression. Since high levels of STRAP proteins are exposed on the cell surface, they are easily targetted by systemically administered agents, and because they are expressed mainly on prostatic epithelial cells, agents targetted to them should have minimal side effects on other tissues.
predicted transmembrane domains, but is encoded by a distinct gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acids may be used for recombinant protein production, as
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Sequence 519 BP; 137 A; 105 C; 102 G; 175 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              benign prostatic hyperplasia; acute prostatitis; testicular cancer;
cryptorchidism; testicular disorder; proliferative disorder; lymphoma;
leukaemla; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
                                                                              112 agctcgtttccatccataaattaaaacatggaaagtacttatgagcagagcgacatatcc 171
                                                                                                                   519 AGCTCGTTTCCATCCATAAATTAAAACATGGAAAGTACTTATGAGCAGAGGGACATATCC 460
                                                                                                                                                          172 aagtgtagactgaataaaactgaattctctccagtttaaagcattgctcactgaagggat 231
                                                                                                                                                                                                  459 AAGTGTAGACTGAATAAAACTGAATTCTCTCCAGTTTAAAGCATTGCTCACTGAAGGGAT 400
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Six-Transmembrane Protein of Prostate 1, STMP1, partial exon 6.
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                                                                                                                                                                                   58.1%; Score 154; DB 21; Length 519; 100.0%; Pred. No. 8.4e-68; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            liver cancer; lung cancer; cytostatic; ds; exon 6.
                                                                                                                                                                                                                                         232 agaagtgactgccaggagggaaagtaagccaagg 265
                                                                                                                                                                                                                                                               399 AGAAGTGACTGCCAGGAGGGAAAGTAAGCCAAGG 366
                100.0%; Pred. No. 8.40
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 AAS15799 standard; DNA; 148 BP
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                                         Matches 154; Conservative
                    Local Similarity
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  Query Match
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Homo sapiens

WO200172962-A2

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testis-specific polypeptides and the nucleic acids encoding them.

testis-specific polypeptides and the nucleic acids encoding them.

Also included are vectors and host cells expressing the proteins, a

transgenic animal expressing the protein, antibodies against the

proteins, probes for detecting the nucleic acids, antisense molecules

for the nucleic acids and methods of isolating modulators of the

proteins. Compounds that modulate the prostate specific or testis

specific polypeptide are useful to diagnose, prevent or treatidisorders

of the testis or prostate particularly prostate cancer, benign

of the testis or prostate particularly prostate cancer, benign

cryptorchidism, undescended, retractile, ascending or vanished

testis. Other proliferative disorders for which the modulators may be

used include lymphoma, leukaemia, melanoma, ovarian cancer, breast

cancer, pancreatic cancer, liver cancer and lung cancer. The

present sequence represents partial exon 6 sequence of a prostate

specific protein, Six-Transmembrane Protein of Prostate 1, SIMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperplasia; acute prostatiis; testicular cancer; cryptorofhidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ds; exon 6; ORF2.
                                                                                                                                                                                                                                                                          prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 ccagaattacaattgagggcaaaacaagagcaaagaacaaagtttggtggtgtataaaatc 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 CCAGAATTACAATTGAGGGCAAAACAAGAGCAAGAACAAAGTTTGGTGGTGTATAAAATC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Six-Transmembrane Protein of Prostate 1, STMP1, ORF2 exon 6.
                                                                                                                                                                                                                                                       polynucleotide for the diagnosis, prevention and treatment for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 148 BP; 36 A; 29 C; 26 G; 57 T; 0 other;
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100.0%; Pred. No. 8.9e-65;
iive 0; Mismatches 0;
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                                                                                            24-MAR-2000; 2000US-191929P.
                                                     23-MAR-2001; 2001WO-US09410
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                                                                                                                                    (SAAT/) SAATCIOGLU F.
                                                                                                                                                                                                                WPI; 2001-662926/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                           Saatcioglu F;
                04-OCT-2001
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Best Local S
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Indels

Pred. No.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The conjudentides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or totreat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as foot supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Ass&4497-AsS&4564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed securing in the contractly from WIPO active to the contract of the contract of the members of the invention of the contract o
Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3900 BP; 1161 A; 798 C; 892 G; 1049 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #104.
                                                                                                                                1346 CTTATGAGCAGAGCGACATATCCAAGTGTAGACTG 1312
                                                                                                   149 cttatgagcagagcgacatatccaagtgtagactg 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 104; 103pp; English.
                                                                                                                                                                                                                                                                                 AAS64300 standard; cDNA; 3900 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631.
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2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
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                                                      transmembrane domain; type IIIa membrane protein; expression; cancer; antigen; immunisation; immune response; cellular; humoral; antigencer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor; drug targetting; recombinant protein; ds.
                                                                                   /purtial
/product= "Human STRAP-2 (serpentine transmembrane
/product= antigen of the prostate)"
/note= "No initiation or termination codons given in
the specification"
                    Gaps
                                         agatccagaattacaattgagggcaaaacaagagcaagaacaagagtttggtggtgtataa 88
                                                                                                                                                                                                                                                                                              Serpentine transmembrane antigen of the prostate; STRAP-2; prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel proteins useful as diagnostic markers and therapeutic targets,
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         2.6e-68;
hes 0;
                                                                                                                              Raitano AB,
                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..519
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           particularly for prostatic cancer
100.08; Pr. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Fig 9; 83pp; English.
                                                                                                                                                                                                           AAZ49398 standard; cDNA; 519
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98US-0091183
                                                                                                                                                                                                                                                                          Human STRAP-2 partial cDNA.
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         Best Local Similarity 100.
Matches 155; Conservative
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RAITANO A B.
SAFFRAN D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hubert RS,
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HUBERT R S.
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                                                                                                                                                                                                                               AAZ49398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUBE/)
(LEON/)
(RAIT/)
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

DNA encoding novel human diagnostic protein #12297.

(first entry)

13-FEB-2002

AAS76493;

AAS76493 standard; cDNA; 2192 BP

RESULT 7

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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules of or the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, oryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence represents the open reading frame of a prostate
    prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                      Denign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ss.
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Human; Six-Transmembrane Protein of Prostate 1; STMP1;
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
178..1650
                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "STMP1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-662926/76.
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Best Local Similarity
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                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                            Key
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -

Tang YT;

Drmanac RT, Liu C, 2001-639362/73.

P-PSDB; ABG12306

(HYSE-) HYSEQ INC.

30-MAR-2001; 2001WO-US08631. 31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.

WO200175067-A2. Homo sapiens.

11-OCT-2001.

Claim 1; SEQ ID No 12297; 103pp; English.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to renerating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical clisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capposible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and animo acid sequences. Asset454 for represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2192 BP; 559 A; 507 C; 551 G; 575 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.5%; Score 155; DB 23;
100.0%; Pred. No. 2.6e-68;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences
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Best Local Simi
Matches 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1390 TGAGCAGAGCGACATATCCAAGTGTAGACTGAATAAAACTGAATTCTCTCCAGTTTAAGG 1331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccagaattacaattgagggcaaaacaagagcaagaacaaagtttggtggtgtataaaatc 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Gaps

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Length 2192; Indels 4

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The present sequence is human six transmembrane epithelial antigen of the prostate (STEAP)-2 clone GTD3 cDNA. STEAP-1 a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is located on chromosome 7q21 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells composition to the patient. Treating a patient with a cancer that composition to the patient. Treating a patient with a cancer that composition to the patient of killing cells expresses STEAP, or inhibiting growth or killing cells expressing STEAP, composition to the patient or killing cells expressing for the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the single chain monoclonal antibody is expressed intracellularly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
 proteins, expressed in human cancers, useful for detecting and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Denign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                 Note: The present sequence is also shown in sequence listing of the specification, but it lacks nulceotides at its 5' end.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 ctgcaaaagatccagaattacaattgagggcaaaacaagagcaagaacaaagtttggtgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 92.1%; Score 244; DB 22; Length 2453; al Similarity 100.0%; Pred. No. 4.1e-113; 244; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2453 BP; 648 A; 537 C; 520 G; 748 T; 0 other;
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178..1650
/*tag= a
                                                     Claim 4; Fig 9A-9D; 187pp; English.
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testis-specific polypeptides and the nucleic acids encoding them.

Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the proteins, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign or prostate proteins, carticularly prostate cancer, benign cryptorchidism, undescended, retractile, ascending or vanished testis other proliferative disorders for which the modulators may be useful cancer, branch and lung cancer, breast cancer, branch and properties are prostate and lung cancer. The present sequence encodes a prostate specific protein, Six-Transmembrane
                                                                                                                                                                                                                                                                                                             prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1510 CCAGAATTACAATTGAGGGCAAAACAAGAGCAAGAACAAAGTTTGGTGGTGTATAAAATC 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212
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                                                                                                                                                                                                                                                                                           New polynucleotide for the diagnosis, prevention and treatment for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 ccagaattacaattgagggcaaaacaagagcaagaacaaagtttggtggtgtataaaatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 tgtagtactcttcctcaaaagctcgtttccatccataaattaaaacatggaaagtactta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 tgagcagagcgacatatccaagtgtagactgaataaaactgaattctctcccagtttaaag
                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to substantially pure prostate-specific or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1330 CATTGCTCACTGAAGGGATAGAAGTGACTGCCAGGAGAAAGTAAGCCAAGG 1278
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 cattgctcactgaagggatagaagtgactgccaggagggaaagtaagccaagg 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ORF of Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1680 BP; 467 A; 334 C; 373 G; 506 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 182; DB 22;
Pred. No. 6.7e-82;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 4E; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS15801 standard; cDNA; 4329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.78;
99.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein of Prostate 1, STMP1
                                                                                     23-MAR-2001; 2001WO-US09410.
                                                                                                                        24-MAR-2000; 2000US-191929P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 232; Conservative
                                                                                                                                                             (SAAT/) SAATCIOGLU F.
                                                                                                                                                                                                                                   WPI; 2001-662926/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                        P-PSDB; AAU10187
             WO200172962-A2.
                                                                                                                                                                                                  Saatcioglu F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JAN-2002
                                                  04-OCT-2001
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AAS15801/c
Dp
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The invention relates to substantially pure prostate-specific or Also included are vectors and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostaticis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence represents the second open reading frame of a prostate specific protein, Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                    Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorochidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ss; ORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                                                                                                                 Human ORF2 of Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2238 BP; 607 A; 457 C; 453 G; 721 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "STMP1, ORF2"
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
188..1552
                                   AAS15810 standard; cDNA; 2238 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAR-2000; 2000US-191929P.
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SAAT/) SAATCIOGLU F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-662926/76.
P-PSDB; AAU10188.
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200172962-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saatcioglu F;
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                              16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2001
                                                                        AAS15810;
RESULT 3
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Human six transmembrane epithelial antigen of prostate-2 clone GTD3 cDNA.
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1352
                                                                                                                                                                                          Orditotar "Human six transmembrane epithelial antigen of the prostate (STEAP)-2, alternative version"
/note= "CDS does not include start and stop codon"
/transl_except= (pos:1714..172, aa.Asp.Ala)
/transl_except= (pos:1834..1842, aa.Arg.Ser)
/transl_except= (pos:1957..1965, aa.Glu-Gly)
/transl_except= (pos:2050..2058, aa.Thr.Ser)
/transl_except= (pos:2050..2058, aa.Thr.Ser)
/transl_except= (pos:2060..2058, aa.Hr.Ser)
/transl_except= (pos:2060..2058, aa.Hr.Ser)
                                                                               201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product- "Human six transmembrane epithelial antigen of the prostate (STEAP)-2"
                                                                                                                142 gaaagtacttatgagcagagcgacatatccaagtgtagactgaataaaaactgaattctct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-2; STEAP-2; chromosome 7q21; cancer; prostate; colon; bladder; lung; ovarian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New STEAP (six transmembrane epithelial antigen of the prostate)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saffran DC,
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/note= "Kozak region"
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352..358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD07072 standard; cDNA; 2453 BP.
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P-PSDB; AAE02781, AAE02841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Jakobovits A;
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Gaps

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0; Indels

Length 2238;

Score 244; DB 22; I Pred. No. 4.1e-113;

92.1%; Scor. 100.0%; Pred. No. ... 0; Mismatches

Conservative

244;

Matches

qq

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Similarity

Query Match Best Local 9

liver cancer; lung cancer; cytostatic; ss; ORF2

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This sequence represents cDNA encoding human prostate growth-associated protein PGAMP-1. Nucleotides encoding PGAMP-1 were initially identified in a prostate cDNA library, this sequence representing a consensus.

Human prostate GDNA library, this sequence representing a consensus.

Human prostate growth associated membrane proteins PGAMP-1 and PGAMP-2

(AAY52590) may be used to raise specific antibodies and to screen for specific modulators (agonists, antagonists or other potential therapeutic agents). Antagonists of PGAMP are used to treat or prevent a vide range of cancers (solid tumours, leukaemla, lymphoma etc.) and reproductive disorders (such as infertility, endometriosis, polycystic ovarian syndrome, prostatitis). PGAMP-encoding nucleic acids, its fragments and complements, may be used for recombinant production of PGAMP proteins, in gene therapy (e.g., as antisense molecules, triplexforming molecules and ribozymes), and as diagnostic probes and primers. Anti-PGAMP antibodies may be used for diagnosts and monitoring of PGAMP-related diseases by standard immunoassays, as therapeutic antibution of antipolis and in containing in the containing molecules and primers and complements.
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                                                                                                                                                                                                       proteins, for treating or -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 ctgcaaaagatccagaattacaattgagggcaaaacaagagcaagaacaagtttggtgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.1%; Score 244; DB 21; I
100.0%; Pred. No. 4.1e-113;
ive 0; Mismatches 0;
                                                                                                                                                                                                                        New human prostate growth-associated membrane
                                                                                                                                                                                                                                                         cancer and reproductive disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS15811/c
ID AAS15811 standard; cDNA; 1561 BP.
                                                                                                                                                                                                                                                                                                                      Claim 7; Page 67; 72pp; English.
                                                            Guegler KJ, Corley NC;
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(INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 244; Conservative
                                                                                                                         WPI; 2000-062671/05
                                                                                                                                                           P-PSDB; AAY52589
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                                                                                                                                                                                                                                                         preventing
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                                                            Lal P,
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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules of or the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer, oryptorchidism, undescende, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be testis. Other proliferative disorders for which the modulators may be cancer, pancreatic cancer, liver cancer and lung cancer, breast cancer, sequence encodes prostate specific protein, Six-Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence encodes prostate specific protein, Six-Transmembrane Protein of Prostate 1, STMP1, ORF2.
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100.0%; Pred. No. 4.1e-113
:ive 0; Mismatches 0;
                                                                                                         /product= "STMP1, ORF2"
                                                            Location/Qualifiers
188..1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 4H; 114pp; English.
                                                                                                                                                                                                        23-MAR-2001; 2001WO-US09410
                                                                                                                                                                                                                                      24-MAR-2000; 2000US-191929P.
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Best Local Similarity 100.
Matches 244; Conservative
                                                                                          /*tag=
                                                                                                                                                                                                                                                                      (SAAT/) SAATCIOGLU F.
                                                                                                                                                                                                                                                                                                                                  WPI; 2001-662926/76.
P-PSDB; AAU10188.
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                              sapiens
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Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hypersplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;

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; Search time 600.75 Seconds (without alignments) 757.357 Million cell updates/sec
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Compugen Ltd.
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                                                                                                 September 20, 2002, 09:59:54
GenCore version
Copyright (c) 1993 - 2000
                                                                OM nucleic - nucleic search, using sw model
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Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human prostate gro	Human cDNA encodin	Human Okf2 Of Six- Human six transmem	Human cDNA encodin	Human ORF of Six-T	DNA encoding novel	DNA encoding novel	Human STRAP-2 part
SUMMARIES		AAS15811	AAD07072	AAS15802	AAS15801	AAS76493	AAS64300	AAZ49398
DB	21	77	7 7 7	22	22	23	23	21
% Query e Match Length DB I	1213	1561	2453	1680	4329	2192	3900	519
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Human Six-Transmem	Human Six-Transmem	Human DNA for Six-	Reverse DNA sequen	Prostate tumour sp	Human immunogenic	Human prostate cDN	Human prostate tum	Human prostate-spe	Human prostate-spe	Prostate tumour an	Reverse DNA seguen	Prostate tumour sp	Human immunogenic	Human prostate cDN	Human prostate tum	Human prostate-spe	Human prostate-spe	Prostate tumour an	Human Six-Transmem	Human Six-Transmem	Human cDNA encodin	Human STRAP-2 gene	SSH fragment cDNA	Human immunogenic	Human prostate cDN	Human prostate-spe	Human prostate-spe	Prostate tumour an	Human Six-Transmem	Human prostate can	Human prostate can			Human breast cance	Human neuroblastom
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55.8	55.8	55.8	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	32.5	32.5	32.5	32.5	32.5	32.5	32.5	32.5	32.1	32.1	15.8	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	8.9	8.9	9.9
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Prostate growth-associated membrane protein; PGAMP-1; prostate; consensus; antibody; screening; modulator; agonist; antagonist; therapeutic agent; cancer; solid tumour; leukaemia; lymphoma; reproductive disorder; infertility; endometriosis; polycystic ovarian syndrome; prostatitis; recombinant expression; gene therapy; antisense therapy; ribozyme; diagnosis; diagnosis; monitoring; immunoassay; targetting; drug delivery; drug screening; ds. Human prostate growth-associated membrane protein PGAMP-1 cDNA. BP. AAZ46296 standard; cDNA; 1213 07-MAR-2000 (first entry) AAZ46296; AAZ46296/c

ALIGNMENTS

Location/Qualifiers 83..508 /*tag= a /product= "Human PGAMP-1" 99WO-US10888 Homo sapiens. W09961469-A2 17-MAY-1999; 02-DEC-1999 Key

98US-0083521.

22-MAY-1998;

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DEFINITION
ACCESSION
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KEYWORDS
SOURCE
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AX155254/c
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Sequence 12 from Patent W00140276.
AX155254
  human.
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Center clone name: 167P22
Center clone name: 167P22
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.99319
Consensus quality: 171178 bases at least Q40
Consensus quality: 171178 bases at least Q30
Consensus quality: 17236 bases at least Q20
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Insert size: 172615; sum-of-contigs
Quality coverage: 12.58x in Q20 bases; agarose-fp
Quality coverage: 9.47x in Q20 bases; sum-of-contigs
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2538: gap of unknown length
8133: contig of 5595 bp in length
8233: gap of unknown length
40378: contig of 32145 bp in length
40478: gap of unknown length
172915: contig of 132437 bp in length.
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RESULT 15
AX140798
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Homo sapiens
Eukaryota; Metazoa; G
Mammalia; Eutheria; E
1 (bases 1 to 301)
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Sequence
AX106507
                                                                                           Sequence
AX140798
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l Similarity 100.0%;
21; Conservative
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Compositions and methods for therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 301)
Xu,J., Skeiky,Y.A., Reed,S.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serpentine transmembrane antigens expressed cancers and uses thereof Patent: Wo 0140276-A 12 07-JUN-2001; Urogenesys, Inc. (US)
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1 (bases 1 to 183)
Afar, D. E., Hubert, R. S., Raitan
Faris, M. and Jakobovits, A.
                                                   human.
                                                                               AX140798.1
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               Chordata;
Primates;
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               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Search completed: September 20, 2002, 09:55:54 Job time: 13212 sec
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                                                                                                                                                      Query Match 7.9%; Score 21; DB 6; Length 301; Best Local Similarity 100.0%; Pred. No. 1; Matches 21; Conservative 0; Mismatches 0; Indels
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                                                                                   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H., Skelky,Y.A. and Wang,A. Compositions and methods for the therapy and diagnosis of prostate cancer patent: WO 0134802-A 288 17-MAY-2001; CORIXA CORPORATION (US)

Location/Qualifiers
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/db_xref="taxon:9606"
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                     Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H., Skeiky,Y.A. and Wang,A. Compositions and methods for the therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                  PAT 29-AUG-2001
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J. compositions and methods for the therapy and diagnosis of prostate
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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8.3e-38;
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Patent: WO 0134802-A 215 17-MAY-2001;
CORIXA CORPORATION (US)
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CORIXA CORPORATION (US)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini; Cercopithecidae, Cercopithecinae, Papio.

Cercopithecinae, Papio.

1 (bases 1 to 172915)

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-O., Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L.-H. and Green, E.D.
                                                                                                                                           Homos apiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Sites)

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.

and Henderson, A. A. A. Hepler, W.T.
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                                                                                                                                                                                                                                                                                                                                                                                           Compositions and methods for the therapy and diagnosis of prostate
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Submitted (20-NOV-2001) NIH Intramural Sequencing Center, 8717
Submitted (20-NOV-2001) NIH Intramural Sequencing Center, 8717
Grovennt Circle, Gaithersburg, MD 20877, USA
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact nisc_mouse@nhgri nih gov
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CORIXA CORPORATION (US)
Location/Qualifiers
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Sequence 215 from Patent WO0173032.
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Green, E.D.
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W.U., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.R., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to.250)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Red,S.G., Kalos,M.D., Fanger,G:R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of prostate
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CORIXA CORPORATION (US)
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Sequence 213 from Patent WO0151633.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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32.5%; Score 86; DB 6; L4
Best Local Similarity 100.0%; Pred. No. 8.3e-38;
Matches 86; Conservative 0; Mismatches 0;
                                                                                                                                   Query Match 35.1%; Score 93; DB 6; Le Best Local Similarity 100.0%; Pred. No. 8.5e-42; Matches 93; Conservative 0; Mismatches 0;
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Sequence 215 from Patent WO0134802. .
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CORIXA CORPORATION (US)
Patent: WO 0173032-A 213 04-OCT-2001; CORIXA CORPORATION (US)
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Sequence 215 from Patent WO0125272.
AXI06434
AXI06434.1 GI:13922113
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/db_xref="taxon:9606"
1. 366
/note="n = A,T,C or G"
a 79 c 69 g 96
                                                                                  69
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Sequencing vector: plasmid: n/a: 100% of reads
Sequencing vector: plasmid: n/a: 100% of reads
Assembly program: Phrap: version 0.990319
Consensus quality: 161001 bases at least 040
Consensus quality: 161422 bases at least 020
Consensus quality: 16152 bases at least 020
Insert size: 143000; agarose-fp
Insert size: 162428; sum-of-contigs
Quality coverage: 10.76x in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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cap of unknown length
contig of 22226 bp in length
gap of unknown length
contig of 29844 bp in length
gap of unknown length
contig of 28876 bp in length
gap of unknown length
gap of unknown length
contig of 2876 bp in length
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Center: NIH Intramural Sequencing Center
Center code: NISC
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Pred. No. 2.6e-45;
0; Mismatches 1;
                           1..16228
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-120K11"
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14023. 36248
/note="assembly_fragment"
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clone_end:T7
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Center clone name: 120K11
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 250)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Sked,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skeiky,Y.A. and Wang,A.
Compositions and methods for the therapy and diagnosis of prostate
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
1 (bases 1 to 250)
2 (Seiky,Y.A., Reed,S.G. and Cheever,M.A.
Compositions and methods for therapy and diagnosis of prostate cancer
Db 116347 TGTAGTACTCTTCTTCAAAAGCTCGTTTCCATCCATAAATTAAAACATGGAAAGTACTTA 116406
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Sequence 213 from Patent W00134802.
AXI40723
AXI40723.1 GI:14280834
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Sequence 213 from Patent WO0125272.
AX106432
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/db_xref="taxon:9606"
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53 c 42 q 69
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53 c 42 g
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               complement(26832. .27124)
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32263 .32563
/rpt_family="ALU"
complement(34737. .7rpt_family="Ll"
36558 .36709
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/rpt_family="PTR" 39839. .40125
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complement(41340.
/rpt_family="ALU"
complement(41904...
                                                                                              27125. .27544
/note="similar to
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44659. .44954
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45422. .45448
/rpt_family="L1"
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10126. .40157
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complement(44380.
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12348. .42409
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WORKING DRAFT SEQUENCE, 6
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Submitted (12-DEC-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
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complement(51721...
/rpt_family="L1"
complement(51765...
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complement(50820.
/rpt_family="THE"
complement(51124.
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51405. 51691
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complement(45672.
/rpt_family="ALU"
complement(45964.
/rpt_family="L1"
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48370. .48785
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complement(49577.
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complement(50540.
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Matches 150; Conservative
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//LABINE ALTON = MESISMMGSPRSLSETCLPNGINGIKDARKYTVGVIGSGDFAKS
//LABINE ALTON = MESISMMGSPRSLSETCLPNGINGIKDALTRUN IFFRAHREHYTSLW
DIRHLLVGKILIDVGKNWRRANGYPESNAEYLASLFPDSLIVKGFNNVSAMALQLGFKD
ASRQVILGNNIQARQOVIPIARAQLANFIPIDGESLSSAREISNLPIRELFTURRGEVVY
AISLAFFFFFLYSFVRDVIHPYRNQSDFYKIPIETVNKTLPIVATTLLSLVYLAGLL
AAAXQLYYGTKYRRFPPWLETWLQCRKQLGILSFFFAMVHVAYSLCLPMRRSERYLFI
NAAXQCYHANIENSWNREEVWRIEMTISFGINSLGLLSLAATSIPSYSNALNWREFS
FIGSTLGYVALLISTFHVLIYGWKRAFFEERYKFYTPPNFVLALVLPSIVLIDLLQLC
RYPD"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 156214)
Gattung, S. and Maggi, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1518 CCAGTTTAAAGCATTGCTCACTGAAGGGATAGAAGTGACTGCCAGGAGGGAAAGTAAAGCC 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1698 CTGCAAAAGATCCAGAATTACAATTGAGGGCAAAAACAAGAGCAAGAACAAAGTTTGGTGG 1639
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Human BAC clone RG016J04 from 7q21, complete sequence.
AC002064
                                                                                                                                                                                                                                                                                                                                              Length 2453;
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Submitted (09-MAY-1997)
Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of H. Sapiens BAC clone RG016J04
Unpublished (1997)
2 (bases 1 to 156214)
                                                                                                                                                                                                                                                                                                                                              Query Match 92.1%; Score 244; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 5.5e-128;
Matches 244; Conservative 0; Mismatches 0;
/note="unnamed protein product"
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e-mail: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                            520 g
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SOURCE
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This sequence was finished as follows unless otherwise noted:

neighboring submissions.

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sections once,

repeat_region

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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send an E-mail to egreen@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                            This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 9788K. For references see: Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996).
all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEICHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of H_RG016J04;
actual end is at 156214 of H_RG016J04. The orientation of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA123941 (NID:91682616)
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19436. .19497
/note="similar to human EST AA123941 (NID:g168261
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/rpt_family="L1"
complement(10000. .11285)
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/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RG016J04"
/clone_lib="CITB-978SK-B"
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complement(9406..9975.\/rpt_fam')
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/rpt_family="ALU"
/complement(977. .1499)
/rpt_family="L1"
3398. .3421
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complement(11315.
/rpt_family="L1"
11666...11687
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complement(25561.
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complement(12010.
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complement(12301.
/rpt_family="L1"
13897. .14096
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15715. .15767
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/rpt_family="L1"
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complement(14777
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5319. .5345
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                                                                                                                                                                                                                                                                                                                                        SOURCE INFORMATION:
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2453)
1 (bases 1 to 2453)
2 (Afar. D.E. Hubbert, R.S., Raitano, A.B., Saffran, D.C., Mitchell, S.C., Faris, M. and Jakobovits, A. Serpentine transmembrane antigens expressed in human prostate cancers and uses thereof
Patent: WO 0140276-A 7 07-JUN-2001;
Urogenesys, Inc. (US)
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fix: sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This sequence was derived from the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2=CM2.HT0323.171
199-033-dlikt3=1999-11-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence start: 7
High quality sequence stop: 404.
                    BE152388 404 bp mRNA linear EST 21-JUN-2000 CMZ-HT0323-171199-033-d11 HT0323 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Print, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 1.5e+02;
0; Mismatches 0;
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/db_xref="taxon:9606"
/clone_lib="HT0323"
/dev_stage="Adult"
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially disested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI Sites. The ligation products were transformed into
BOORI Sites and the side of the s
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                                                                                                                                              Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jone
(pieterédejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 307 row: I column: 3
Seq primer: T7
Class: BAC ends.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Cother_GSSS: RCCI-23.30713.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for G
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Pred. No. 1.5e+02;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: September 20, 2002, 08:33:51
Job time: 8715 sec
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100.0%; Pr
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                                                                                         (bases 1 to 493)
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Gaps

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1 (bases 1 to 377)
Hiller, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
A., M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E.,
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="female"
/dev_stage="49 year old"
/lab_host="80LR cells (kanamycin resistant)"
/lab_host="SoLR cells (kanamycin resistant)"
/site_1: Xhot; cloned unidirectionally. Primer: Oligo dT.
Site_2: Xhot; cloned unidirectionally. Primer: Oligo dT.
Total ovary tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GAATTCGGCAGGG 3' ~3' adaptor sequence: 5'
                                                                                                                                                                                                                                  T53018 377 bp mRNA linear EST 06-FEB-1995 ya82h06.sl Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:68219 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High gality sequence stops: 345 Source: IMAGE Consortium, LLNL The clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 377;
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                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:68219"
/clone_lib="Stratagene ovary (#937217)"
/sex="female"
             Pred. No. 1.6e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.4%; Score 19; DB 10; 100.0%; Pred. No. 1.5e+02; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:504476"
/db_xref="taxon:9606"
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100.08; Pr
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                                                                                472 tcagtgagcaatgctttaa 490
                                                                                                        231 TCAGTGAGCAATGCTTTAA 213
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                                                                                                                                                                                                                                                                                                                             T53018.1 GI:654878
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                                       Conservative
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Matches 19; Conserv
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JOURNAL
MEDLINE
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KEYWORDS
SOURCE
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T53018
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//clone_lib="Ra147.1"
/note="Vector: Lambda ZAPII; Physiological conditions:
cycling cells one hour post-inoculation with X.campestris
pv campestris strain 147 in the presence of cycloheximide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 306)
         Dmail: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genelics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Bag or row: D column: 8
Seg primer: T7
Class: BAC ends
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100.0%; Pred. No. 48;
.ive 0; Mismatches 0; Indels
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UMROS CNRS/INRA
BP 27,31326 Castanet-Tolosan cedex,France.
Email: roby@toulouse.inra.fr.
Location/Qualifiers
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/strain="ecotype columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                     High quality sequence stop: 488.
Location/Qualifiers
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Matches 20; Conservative
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TITLE
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mahairas, G.G., Waliace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS 27-AUG-1999
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 488)
                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HS_5304_B2_B04_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=880 Col=8 Row=D, DNA sequence.
AQ833520
AQ833520.1 GI:5799582
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                                                                                                                                                                                                               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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High Throughput Sequencing Center
University of Washington
VOI Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 380;
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                                                                                                        The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M.Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 329.
Location/Qualifiers
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Pred. No. 49;
0; Mismatches
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Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vj29c03.rl Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:930436 5', mRNA sequence.
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 261)
1 (bases 2 to 261)
1 (bases, Gardan, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivelar, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMZ&t2=PMZ-AN0093-
151000-003-a09&t3=2000-10-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 3
High quality sequence start: 3
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musil
1 (bases 1 to 380)
      PM2-AN0093-151000-003-a09 AN0093 Homo sapiens CDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                          \label{eq:simpson,A.J.} Shotgun sequencing of the human transcriptome \ \mbox{with ORF expressed}
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Pred. No. 51;
0; Mismatches 0;
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Corganism="Homo sapiens"
/db_xref="taxon:9606"
/clone_11b="AN0093"
/dev_stage="Adult"
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100.0%; Pre
0;
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AA511666.1 GI:2249520
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2608017"
/clone_lib="CITBI-E1"
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Best Local Similarity 100.0%; Pred. No.
Matches 21; Conservative 0; Mismatc)
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Best Local Similarity
Matches 20; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 627)

E Taegaye, G. Ger, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., Ge Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

Contact: Shaying Jhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPCI-24-256N22.TV RPCI-24 Mus musculus genomic clone RPCI-24-256N22 , DNA sequence.
BH067591
BH067591.1 GI:14886972
GSS.
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pdeJong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 256 row: N column: 22
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                     /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="Solls"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="RPCI-24-256N22"
/clone_lib="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pTARBACI; Site_1: BamH1; Site_2: BamH1;
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                 Score 22; DB 9; Length 728;
Pred. No. 4.6;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                               2 others
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzgechgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. .728
/db_xref="taxon:9606"
/clone="GLCADC12"
/clone="GLCADC12"
/clone="GLCADC12"
/clone="GLCADC12"
/clone="GLCADC12"
/clone="GLCADC12"
/clone="GLCADC12"
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                                                                                                                                                                                                                                                                                                                                                                 3.9%; Scontilarity 100.0%; Proceed Conservative 0;
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Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                             214
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 198)
S 2hao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CITBI-EL-2608017.TR CITBI-El Homo sapiens genomic clone 2608017, DNA sequence.
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RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA "
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Seg primer: M13 Reverse
Class: BAC ends.
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/cel_type="sperm"
/cole="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
/note="Vector: pBeloBAC11; Site_1: EcoR1; Caltech Human BAC Library D"
caltech Human BAC Library D"
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red. No. 15;
Mismatches 0; Indels
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52;
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tive 0; Mismatches
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Query Match 3.9
Best Local Similarity 100.
Matches 22; Conservative
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 497)
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AQ406733 408_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=679 Col=16 Row=B, DNA sequence.
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Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E., Sensen,C.W.,
P.M.K. and Moore,S.S.
Gene Expression Profiling of the Bovine Gastrointestinal
Unpublished (2002)
Unpublished (2002)
Beef Genomics Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9913"
/clone_lib="Bos taurus Duodenum #1 library"
/tissue_type="Smooth muscle"
/cell_type="Simple columnar epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 558;
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Pred. No. 1.6e-06;
0; Mismatches 0;
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Insert Length: 558 Std Error:
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Conservative 0;
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AQ406733.1 GI:4429355
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Homo sapiens
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/note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites" 9 others
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.
I (bases 1 to 728)
Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cat, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma
                                                                                                                                                                                                                                                   High Throughput Sequencing Center University of Washington (University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3887
Email: juallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (Pieter&dejong.mad.buffalo.edu, Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
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                                                                             Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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/db_xref="taxon:9606"
/clone="plate=679 col=16 Row=B"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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Pred. No. 4.8;
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                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC, Hood L
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Location/Qualifiers
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Plate: 679 row: B column: 16
Seq primer: T7
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llni.gov/bbrp/image./image.html
Insert Length: 305 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham.
Location/Qualifiers
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intraepithelial neoplasia (low-grade), cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5381."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 393)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
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Email: cgapbs-rêmail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                 155 ttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttggt 214
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0
                                                                                                                                                                        Score 174; DB 9; Length 322;
Pred. No. 1.3e-75;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="INAGE:163629"
/clone_lib="NCL_CGAP_Kid3"
/lab_host="DH10B"
                                                                                             62 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
AI016724
AI016724.1 GI:3231060
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99.6%;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Manmalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.

Tel (bases 1 to 595)

Stone, R.T., Heaton, W.P., Gross, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.

Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine

Uppublished (2000)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the minscore 18 and -minmatch 12 options.
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of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. " 84 c \, 61 g \, 116 t
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                                                                                                                                           Length 393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ьтээчээ/
384188 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BI359597
                                                                                                                                                                                   Indels
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                                                                                                                                      DB 9; Le
3e-52;
hes 0;
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6.8e-29;
                                                                                                                                      22.7%; Score 127; DB
100.0%; Pred. No. 3e-
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sus scrofa"
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/lab_host="DH10B"
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Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI359597.1 GI:15055625
                                                                                                                                        Query Match 22.7%
Best Local Similarity 100.0
Matchés 127; Conservative
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BI133492 UI-M-BH3-BI845092 fq35c10.y BM035184 fu40c11.y AQ567312 HS_110_B BI864123 ft15b04.y AV933870 AV933870

B1864118 ft133070 B1748868 RPCT-24-8 B172993 ft24e01.y B172993 ft24e01.y B17393 ft24e01.y B183566 ft33h04.y B183566 ft33h04.y B1428484 ft28412.y AA905417 fj59b06.y AA905417 fj59b06.y AA913 RPCT-24-2 B1704176 zfshTARAM B1704176 zfshTARAM B1704176 zfshTARAM B1704176 zfshTARAM B1704176 zfshTARAM B1704176 zfshTARAM B182063 60246669 B182063 60246669 B18465003 AGENCOURT

AA123941 mq22f09.r AW902857 QV3-NN102 AW690320 NF029D05S AA524308 ng32h12.s

```
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Trissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llhi.gov/Darp/image/image.html
Insert Length: 1000 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 249.
Location/Qualifiers
1. .322
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/clone="ImAGE:941693"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AA508880 322 bp mRNA linear EST 13-AUG-1997 ng86f03.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:941693, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 322)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                    AV933870
BI864118
AZ74868
BI472993
AZ790856
AZ939466
BI839566
BI839566
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AQ59620
AZ897813
B1704176
BG522063
CNS02MZK
B10678
B08494
BM455003
                                                                                                                                                                                                                                                                                                     AA123941
AW902857
AW690320
AA524308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
AA508880
AA508880.1 GI:2245821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
RESULT 1
AA508880
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
ORGANISM
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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AA508880 ng86f03.s
A1016724 ov03d03.x
B1359597 384188 MA
BM431438 1Du016F03
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BH067591 RPCI-24-2
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T53018 YAB2H06.s1
BE152388 CM2-HT032
AQ83977 RPCI-23-3
B1350655 fr44h06.y
                                                                                                (without alignments)
1495.679 Million cell updates/sec
                                                                                    Search time 5053.42 Seconds
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                                                                                                                                                               1 acatttttttttccttgatgc......stcataagtactttccatgt 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                              27472414
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                          13736207 segs, 6748477542 residues
                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                    September 20, 2002, 08:33:47
                                                                                                                                                                                                                                                                                                                                             summaries
                                                           - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI016724
BI359597
BM411438
AQ406733
AV646697
AP64697
BP053741
AP53741
AA511666
AQ833520
Z24497
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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em_gss_hum:*
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Minimum DB seq Maximum DB seq

Database :

Word size :

Searched:

Perfect score:

Title:

Sequence:

OM nucleic

Run on:

Scoring table:

T53018 BE152388 AQ983972 BI350635 BM034788

127 80 80 22 22 22 20 20 20 20 119 119

10 11 11 11 11 11 11 11 11

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Result

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                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MAILOR, Vincent J.
APPLICANT: MAILOR, Vincent J.
APPLICANT: MAILOR, Michael B.
APPLICANT: MAICHAEL G.
APPLICANT: MAICHAEL G.
APPLICANT: WAICHELL, GATY
APPLICANT: WAICHELL B.
CORRESPONDENCES: 33
CORRESPONDENCES: 33
CORRESPONDENCES: 33
CORRESPONDENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STRET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10036/2711
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: O1-APR-1994
CLASSIFICATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 31
NAME: COLUZI, LAURA A
REGISTRATION NUMBER: 30,742
RELECHONE: (212) 790-9090
TELECHOWNUICATION INPORMATION:
TELEX: 6121 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1515 base pairs
3.0%; Score 17; DB 4; Length 511; 100.0%; Pred. No. 21; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                   Sequence 1, Application US/08221816B Patent No. 5738985
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 1359 AATGAGGAAGAAGTTTG 1375
                                                                                        379 aatgaggaagaagtttg 395
Query Match 3.0
Best Local Similarity 100.
Matches 17; Conservative
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EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11:
MOLECULE TYPE:
                                                                                                                                                                                                          RESULT 15
US-08-221-816B-1
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Search completed: September 20, 2002, 09:51:16 Job time: 11864 sec ö

Gaps

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DB 4; Length 17138; 6.4; Indels

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES: 666
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EE: PANITCH SCHWARZE JACOBS & NADEL, P.C. ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FLR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.2%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 6.4 Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PROCKOP, DARMIN J.
APPLICANT: SPOTILA, LORETTA D.
APPLICANT: SEREDA, LARISA
APPLICANT: SEREDA, LARISA
APPLICANT: LARSON, ANDREA W.
APPLICANT: PACK, MICHAEL
APPLICANT: COLIGE, ALAIN
APPLICANT: EARLY, JAMES
APPLICANT: KORKKO, JARMO
APPLICANT: ALA-KOKKO, LEENA, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 141, Application US/08943731 Patent No. 6265157 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
; NAME/KEY: misc_feature; LCCATION: (1)...(17138); OTHER INFORMATION: n = A,T,C or G US-09-920-048-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: DNA (genomic) US-08-943-731-141
                                                                                                                                                                                                                                                                                                                     282 tgcctacagcctctgctt 299
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TYPE: nucleic acid
STRANDEDNESS: double
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TELEX: 831-494
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 215-500
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ZIP: 19103-7086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-943-731-141/C
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GENERAL INFORMATION:

APPLICANT: MERKULOV, Gennady et al

TITLE OF INVENTION: ISOLATED HUMAN PROFEASE PROTEINS,

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CLOO1177

CURRENT APPLICATION NUMBER: US/09/813,819

CURRENT APPLICATION NUMBER: US/09/813,819

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09920048
Patent No. 6344352
GENERAL INFORMATION
ENTRY CONTROL OF CONTROL
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                                                                                                                                                                                                                                                      Score 18; DB 4; Length 2081;
Pred. No. 6.5;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09813819 Patent No. 6294368
                                                                                                                                                                                                                                                      Query Match 3.2%; Soc
Best Local Similarity 100.0%; Pi
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)...(17138)
; OTHER INFORMATION: n = A,T,C or
US-09-813-819-3
                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                      2862 TGCCTACAGCCTCTGCTT 2845
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                                                                                                                                       ; LOCATION: 1..2081
US-08-235-836C-71
                                                                                                               NAME/KEY: CDS
STRANDEDNESS:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 17138
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US-09-920-048-3/c
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MOLECULE TYPE: DNA (genomic)
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                                           APPLICATION NUMBER: US 0:
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 agctgcttatcaacttta 179
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INFORMATION FOR SEQ ID NO: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Upton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 11973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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US-08-235-836C-67
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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Patent No. 6248562
GENERAL INFORMATION:
APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrella Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                                        APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
APPLICANT: Steven G.
APPLICANT: Ralos, Mitcheel
APPLICANT: Ralos, Mitcheel
APPLICANT: Ralos, Mitcheel
APPLICANT: Ralos, Mitcheel
APPLICANT: Ralos, Cary
APPLICANT: Retter, Mark
APPLICANT: Bolk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: OMPOSITIONS OF PROSTATE CANCER
FILE REPERBENCE: 210121 427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 214
LENGTH: 444
TYPE: DNA
ORGANISM: HOMO Sapien
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100.0%; Pred. No. 6.1e-15;
                           388 ATTGTGAATAAAACCTTACCTATAGTTGCCATTACTTTGCTCTCCCTA 435
91 attgtgaataaaaccttacctatagttgccattactttgctctcccta 138
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.6%; Score 48; DB Best Local Similarity 100.0%; Pred. No. 6.1 Matches 48; Conservative 0; Mismatches
                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Hicham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Tang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Michael
                                                                                                                                                      Sequence 214, Application US/09439313 Patent No. 6329505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : NAME/KEY: misc_feature

: LCCATION: (1)...(444)

: OTHER INFORMATION: n = A,T,C or G

US-09-439-313-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS AMPLED PATTONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 11973
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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Gaps
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APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 4;
Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                 NAME: BOGOSIAN, MATGATET C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION INFORMATION:
TELEPRAX: (516) 282-7338
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 2081 base pairs
US 08/148,191
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US-08-235-836C-71/C
; Sequence 71, Application US/08235836C
; Patent No. 6248562
; GENERAL INFORMATION:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MARGATEC.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BML9
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 100.0%; Pi
Matches 18; Conservative 0;
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Length 250;

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342 ttatcagcaggttcatgcaaatattgaaaactcttggaatgaggaagaagtttggagaat 401
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23.6%; Score 132; DB 4;
Best Local Similarity 99.5%; Pred. No. 4.8e-57;
Matches 182; Conservative 0; Mismatches 1
                               ; LOCATION: (1)...(250)
; OTHER INFORMATION: n = A,T,C or
US-09-439-313-213
                NAME/KEY: misc_feature
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; MOLECULE TYPE:
US-09-030-607-214
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28 ACT 26
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STATE: WA
COUNTRY:
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APPLICANT: MILCIDAM, JOHNITHER L.,
APPLICANT: Hardocker, Susan Louise
APPLICANT: Reded, Steven G.
APPLICANT: Fanger, Gary
APPLICANT: Fanger, Gary
APPLICANT: Barker, Mark
APPLICANT: Bolk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42709
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT APPLICATION NUMBER: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 132; DB 4; Length 250;
Pred. No. 4.8e-57;
0; Mismatches 1; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION: 25-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVId J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6011
INFORMATION FOR SEQ ID NO: 213:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INCREMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Reed, Steven G.
APPLICANT: Relos, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 213, Application US/09439313 Patent No. 6329505
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.6%;
Best Local Similarity 99.5%;
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: CDNA
US-09-030-607-213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapien
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ACT 26
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LENGTH: 250
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APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun C. APPLICANT: Dillon, Davin C. TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPALIABLE
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 2-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                               ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 base pairs
TYPE: nucleic acid
Sequence 214, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
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                            285 TTCGCTATGGTCCATGTTGCCTACAGCCTCTGCTTACCGATGAGAAGGTCAGAGATAT 226
                                                                                                                                          325 ttgittctcaacatggcttatcagcaggttcatgcaaatattgaaaactcttggaatgag 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385 gaagaagtttggagaattgaaatgtatatctcctttggcataatgagccttggcttactt 444
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                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Xu, Jangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Hatchex, Susan Louise
APPLICANT: Hatchex, Susan Louise
APPLICANT: Hatchex, Susan Louise
APPLICANT: Redes, Steven G.
APPLICANT: Redes, Steven G.
APPLICANT: Redes, Mitcheel
APPLICANT: Retter, Mark
APPLICANT: Retter, Mark
APPLICANT: Control Conformation Compositions and Methods For THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICANT: 1999-11-12
NUMBER OF SEO ID NOS: 575
SOUTRARE: FRASESQ for Windows Version 3.0
SEO ID NO 215
LENTH: 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                        Sequence 215, Application US/09439313
Patent No. 6329505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)...(366)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-215
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LOCATION: (1)...(366)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                        Patent No.
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ATHLE E. Raitano
APPLICANT: ATHLE E. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: EXRESSED IN HUMAN CANCERS AND USES THEREOF
TITLE REFERENCE: 129.1609U2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 174; DB 4; I
Pred. No. 4.2e-78;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 213, Application US/09030607; Patent No. 6262245
                                                                                                   US-09-323-873A-9; Sequence 9, Application US/09323873A; Patent No. 6329503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.1%;
99.6%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.6
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo Sapiens
45 AGTTTTATTCAGT 33
                                                                                                                                                                                                                                               Kahan Leong
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                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 9
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249 attactaagttttatcttcgctatggtccatgttgcctacagcctctgcttaccgatgag
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 215, Application US/09030607 Patent No. 6262245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
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99.6%;
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 36.1
Best Local Similarity 99.6
Matches 252; Conservative
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STATE: WA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Greley, Neil C.
TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPER EPIOPPY disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PEFFECT 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
PFILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 321; DB 3; I
Pred. No. 8.7e-152;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/ACENT INFORMATION:
NAME: CERRONE, MICHEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-05
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1213 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                             US-09-083-521-3; Sequence 3, Application US/09083521; Patent No. 6048970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.3%;
99.7%;
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Best Local Similarity 99.7
Matches 371; Conservative
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LIBRARY: PROSTU
CLONE: 1691243
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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                                   368
                                                         428
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                                                                                                                                                                                                                                                                            265 ttcgctatggtccatgttgcctacagcctctgcttaccgatgagaaggtcagagaatat 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                aaactcttggaatgaggaagaagtttggagaattgaaatgtatatctcctttggcataat
61 ATTACTAAGTTTTTTCTTCGCTATGGTCCATGTTGCCTACAGCCTCTGCTTACCGATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 202; DB 4;
Pred. No. 3.9e-92;
0; Mismatches 1.
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TELECOMMUNICATION INFORMATION:
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Sequence 56, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 12, Appl
Sequence 132, Appl
Sequence 132, Appl
Sequence 1, Appli
Sequence 1070, Appli
Sequence 1072, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rahan Leong
APPLICANT: Rahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTINE
TITLE OF INVENTION: NOVELS SERPENTINE
TITLE OF INVENTION: NOVERER: US/09/323,873A
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
SPRIOR FILING DATE: 1998-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 521;
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           US-08-832-883-56
US-08-832-883-56
US-08-832-877-56
US-08-836-2614-1
US-08-836-261-810-132
US-08-951-92
US-08-952-902D-132
US-08-121-446-3
US-08-121-446-3
US-08-131-1446-3
US-08-131-13
US-08-131-13
US-08-131-13
US-08-131-134
US-08-137-124A-1070
US-08-373-124A-1070
US-08-373-124A-1070
US-08-373-124A-1070
US-08-373-124A-1070
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US-08-373-124A-1070
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                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09323873A Patent No. 6329503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.8
Matches 494; Conservative
                                   837
1842
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2687
2687
2771
4301
4852
5160
72928
87350
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US-09-323-873A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-323-873A-7
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984.292 Million cell updates/sec
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215, App
215, App
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71, Appl
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560
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/FQTC_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTC_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTC_COMB.seq:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-439-313-215

US-09-439-313-213

US-09-439-313-213

US-09-439-313-214

US-09-439-313-214

US-09-439-313-214

US-09-235-836C-67

US-09-920-048-3

US-08-943-11-141

US-08-943-11-141

US-08-943-11-141

US-08-943-11-141

US-08-143-21-141

US-08-143-21-141

US-08-143-141

US-08-143-141

US-08-143-144-4

US-09-141-228-4

US-09-341-228-4

US-09-341-228-1

US-08-943-731-3

US-08-943-731-3

US-08-943-731-3

US-08-943-731-3

US-08-943-731-3

US-08-943-731-3

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US-08-943-731-3

US-08-943-731-3

US-08-682-218-11
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                                                                                                                                                                                                                                                                                                                                        383533 seqs, 122816752 residues
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                                                                                          nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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          The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperstalia; acticular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises
                                                                                                                                                                                                                                                                     ttoctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctag 139
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                                                                                                                        Length 395;
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                                                                                   Sequence 395 BP; 100 A; 84 C; 80 G; 131 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         liver cancer; lung cancer; cytostatic; ds; exon 4.
                                                                                                                      Score 282; DB 22;
Pred. No. 4.2e-135;
); Mismatches 1;
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Best Local Similarity 99.7%;
Matches 332; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS15797 standard; DNA; 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JAN-2002
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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them.

Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign of the testis or prostate prostatilis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, preast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence represents exon 4 of a prostate specific protein, Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tatacctcgcaggtcttctggcagctgcttatcaactttattacggcaccaagtatagga 199
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                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Length 528;
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prostate-specific or testis-specific nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                           Score 281; DB 22;
Pred. No. 1.4e-134;
0; Mismatches 1;
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                              Fig 4C; 114pp; English.
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nilarity 99.7%;
Conservative 0
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Matches 331;
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139 182 259

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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe #5437 for gene expression analysis in human cervical cell sample.
                                                                                          243 gatttccaccttggttggaaacctggttacagtgtagaaaacagcttggattactaagtt 302
                                                                                                                                                                                                                   Probe; human; microarray; gene expression; cervical epithelial cell;
                                                     gatttccaccttggttggaaacctggttacagtgtagaaaacagcttggattactaagtt
                                         ttcctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctag
                                                                                                                                                                                                      ttatcttcgctatggtccatgttgcctacagcctctgcttaccgatgagaaggtcagaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                       363 gatatttgtttctcaacatggcttatcagcagg 395
                                                                                                                                                                                                                                                         320 gatatttgtttctcaacatggcttatcagcagg 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID No 5437; 487pp; English.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-02369.
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                                                                                                                                                                                                                                                                                                                                                      AAI15504 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cervical cancer; ss.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                          sample.
                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
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                                     Length 395;
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                         microarray; human; placenta; antenatal diagnosis;
               80 G; 131 T; 0 other;
                                      ; DB 22;
4.2e-135;
                                      Score 282; DB Pred. No. 4.2e 0; Mismatches
                                                                                                                                                                                                                                  SEQ ID No 5608; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank DR;
                                                                                                                                                                                                                                                                                           BP.
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              Sequence 395 BP; 100 A; 84 C;
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                                      50.4%;
ilarity 99.7%;
Conservative
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2000US-0608408.
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                                                                                                                                                                                                                                                                                           standard;
                                      Query Match
Best Local Similarity
Matches 332; Conserv
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
04-OCT-2000;
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03-AUG-2000;
21-SEP-2000;
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Best Local Simil
Matches 332; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                      human
ttatcttcgctatggtccatgttgcctacagcctctgcttaccgatgagaaggtcagaga 319
         ttcctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctag 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                     numan; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO: 5403; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                          Human brain expressed single exon probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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Pred. No. 4.2e-135;
0; Mismatches 1;
                                              gatatttgtttctcaacatggcttatcagcagg
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2000US-0207456.
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2000GB-0024263.
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ilarity 99.7%;
Conservative
                                                                                                    AAK05412 standard; DNA; 395
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                                                                                                                                         (first entry)
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Matches 332; Conserv
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27-SEP-2000;
04-OCT-2000;
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302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression analysis; probe;
                                                  ttatcttcgctatggtccatgttgcctacagcctctgcttaccgatgagaaggtcagaga
                                                                            genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human bone marrow expressed single exon probe SEQ ID NO: 5568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; bone marrow expressed exon; gene expression ar
microarray; cancer; leukaemia; lymphoma; myeloma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 G; 131 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 282; DB 22;
Pred. No. 4.2e-135;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analyzing gene expression in human bone marrow
                                                                                                                                                320 gatatttgtttctcaacatggcttatcagcagg 352
                                                                                                                                                                                                395
                                                                                                                                                                          DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank
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                                                                                                                                                                                                                                                                                                                        BP
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2000US-0207456.
2000US-0608408.
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                                                                                                                                                                                                                                                                                                                        AAK31011 standard; DNA; 395
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the probes of the invention
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measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, endicying and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                    Probe #5375 for gene expression analysis in human heart cell sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.4%; Score 282; DB 22; Length 395; 99.7%; Pred. No. 4.2e-135;
                                                                                                                     expression; heart; microarray; vascular system; ar disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 395 BP; 100 A; 84 C; 80 G; 131 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 5375; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                        congenital heart disease; ss.
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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2000US-0608408
                                                   (first entry)
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Matches 332; Conservative
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Best Local Similarity
                                                                                                                                                                                                                            WO200157274-A2.
                                                                                                                       Human; gene exp
cardiovascular
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30-JUN-2000;
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                                                                                                                                                                                             Homo sapiens
                                                   23-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tatacctcgcaggtcttctggcagctgcttatcaactttattacggcaccaagtatagga 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 5682; 639pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 395 BP; 100 A; 84 C; 80 G; 131 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 282; DB 22;
Pred. No. 4.2e-135;
                                                                                                                                                                                                                                                                                                                                                                                                                         analyzing gene expression in human fetal liver
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                                                                                                                                                                                                                                                                                                                                   Rank DR;
                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                      2000US-0180312.
2000US-0207456.
2000US-0608408.
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2000US-0234687.
2000US-0236359.
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                                                                                                                     30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                             04-OCT-2000; 2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                 WO200157277-A2.
                                                                                                                                                                                                          03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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Query Match Best Local S

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ABA26909 RESULT

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Gaps 79

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protein PGAMP-1. Nucleotides encoding pGAMP-1 were initially identified in a prostate cDNA library, this sequence representing a consensus. Human prostate growth associated membrane proteins PGAMP-1 and PGAMP-2 where in proteins pGAMP-1 and pGAMP-2 where are also to raise specific antibodies and to screen for specific modulators (agonists, antagonists or other potential cherapeutic agents). Antagonists of PGAMP are used to treaf or prevent a wide range of cancers (solid tumours, leukaemia, lymphoma etc.) and reproductive disorders (such as infertility, endometriosis, polycystic ovarian syndrome, prostatitis). PGAMP-encoding nucleic acids, its fragments and complements, may be used for recombinant production of pGAMP proteins, in gene therapy (e.g., as antisense molecules, triplexforming molecules and ribozymes), and as diagnostic probes and primers.

Comming molecules and ribozymes), and as diagnostic probes and primers.

Anti-PGAMP antibodies may be used for diagnostic probes and primers.

Comming molecules and ribozymes), and as diagnostic probes and primers.

Anti-PGAMP antibodies may be used for diagnostic probes and primers antagonists (including targetted delivery of other drugs), and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                     represents cDNA encoding human prostate growth-associated
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 1213 BP; 335 A; 239 C; 215 G; 424 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 321; DB 21;
Pred. No. 3.5e-155;
                                               prostate growth-associated membrane
                                                           and reproductive disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                       Claim 7; Page 67; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                      57.3%;
99.7%;
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             consensus; antibody; screening; modulator; agonist; antagonist; therapeutic agent; cancer; solid tumour; leukaemia; lymphoma; reproductive disorder; infertility; endometriosis; polycystic ovarian syndrome; prostatitis; recombinant expression; gene therapy; antisense therapy; ribozyme; diagnosis; diagnosis; monitoring; lumunoassay; targetting; drug delivery; drug screening;
                                            cctttgtcagagatgtgattcatccatatgctagaaaccaacagagtgacttttacaaaa
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                 Indels
Pred. No. 3.8e-171;
): Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human PGAMP-1"
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99.68;
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              Matches 452; Conservative
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AAS15813
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                                                                                                                                                                         testis-specific polypeptides and the nucleic acids encoding them.
Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign of the testis or prostate particularly prostate cancer, benign or prostatic hyperplasia, acute prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, there are represents the cancer, liver cancer, liver cancer and lung cancer. The present sequence represents the open reading frame of a prostate specific protein, Six-Transmembrane Protein of Prostate 1, STMP1.
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                                                                                                                prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
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                                                                                                      New polynucleotide for the diagnosis, prevention and treatment for
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                                                                                                                                                                  The invention relates to substantially pure prostate-specific or
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Pred. No. 1.1e-189;
); Mismatches 3;
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99.4%;
         24-MAR-2000; 2000US-191929P.
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Matches 538; Conservative
                                (SAAT/) SAATCIOGLU F.
                                                                       WPI; 2001-662926/76.
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                                                    Saatcioglu F;
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DB 22; Length 2102;

Score 352;

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testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatiis, testicular cancer, ryptorchidism, undescended, retractile, ascending or vanished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence encodes a prostate specific protein, Six-Transmembrane
                                                                                                                                                                                                                                                                                                                                                    Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; beniugn prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
                     1523 aattcagttttattcagtctacacttggatatgtcgctctgctcataagtactttccatg 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                                                                                                                                                                                                                                                                                 Human cDNA encoding Six-Transmembrane Protein of Prostate 1, STMP1.
 aattcagttttattcagtctacacttggatatgtcgctctgctcataagtactttccatg
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                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; lung cancer; cytostatic; ss.
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178..1650
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Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
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Length 1680;
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                   Indels
Score 388; DB 22;
Pred. No. 1.1e-189;
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; Mismatches
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69.3%;
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                                                                                                         gaaaactcttggaatgaggaagaagtttggagaattgaaatgtatatctcctttggcata 360
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                                                                                                                                                                                                                                                                                  Human six transmembrane epithelial antigen of prostate-2 clone GTD3
                             accaagtataggagatttccaccttggttggaaacctggttacagtgtagaaaacagctt
       agaaggtcagagagatatttgtttctcaacatggcttatcagcaggttcatgcaaatatt
                                                                                                                       gaaaactcttggaatgaggaagaagtttggagaattgaaatgtatatctcctttggcata
                                                                                                                                                                                                                                                                                               Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-2; STEAP-2; chromosome 7q21; cancer; prostate; colon; bladder; lung; ovarian;
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/note= "Kozak region"
                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                     AAD07072 standard; cDNA; 2453 BP.
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187
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The present sequence is human six transmembrane epithelial antigen of the prostate (STEAP)-2 clone GTD3 CDNA. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is located on chromosome 7q21 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and parcreatic) expressing STEAP or inhibiting growth or killing cells expressed STEAP, or inhibiting growth or killing cells composition to the patient. Treating a patient with a cancer that composition to the patient. Treating a patient with a cancer that composition to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, course that the vector delivers the single chain monoclonal antibody is expressed intracellularly.
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                                                                                                                                                                                                                                                         New STEAP (six transmembrane epithelial antigen of the prostate) proteins, expressed in human cancers, useful for detecting and treating
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                                                                                                  Faris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The present sequence is also shown in sequence listing of the specification, but it lacks nulceotides at its 5' end.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2453;
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                                                                                                  Saffran DC,
                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 9A-9D; 187pp; English.
                                                                                                     Raitano AB,
99US-0455486
                                                                                                                                                                                                           P-PSDB; AAE02781, AAE02841.
                                                 (UROG-) UROGENESYS INC
                                                                                                     Hubert RS,
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                                                                                                                              Jakobovits
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98US-0087520. 98US-0091183.

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30-JUN-1998;
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                                                                                                                                                         tactttccctcctggcagtcacttctatcccttcagtgagcaatgctttaaactggagag 1355
                                                                                                                                                  gatatttgtttctcaacatggcttatcagcaggttcatgcaaatattgaaaactcttgga 379
                                                                                                                                                                                                                                                                                                                                                                                           Serpentine transmembrane antigen of the prostate; STRAP-2; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; antigen; immunisation; immune response; cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor; drug targetting; recombinant protein; ds.
       cctttgtcagagatgtgattcatccatatgctagaaaccaacagagtgacttttacaaaa 935
                                                      tatacctcgcaggtcttctggcagctgcttatcaactttattacggcaccaagtatagga 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product- "Human STRAP-2 (serpentine transmembrane antigen of the prostate)"
/note= "No initiation or termination codons given in the specification"
                                     936 ttcctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctag
                                                                                                                                                                                                             tactttccctcctggcagtcacttctatcccttcagtgagcaatgctttaaactggagag
                      ttcctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctag
                                                                                                                   ttatcttcgctatggtccatgttgcctacagcctctgcttaccgatgagaaggtcagaga
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               AAZ49398 standard; cDNA; 519 BP.
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                                                                                                                                                                                                                                                                                                                                                                             Human STRAP-2 partial cDNA.
                                                                                                                                                                                                                                                                                                                                                               (first entry)
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This sequence represents a partial CDNA encoding a novel human protein, STRAP-2 (serpentine transmembrane antigen of the prostate). STRAP-2 is chighly bemologous to STRAP-1 (AAYSB194), particularly throughout the predicted transmembrane domains, but is encoded by a distinct gene, predicted transmembrane domains. but which show no significant structural conservation, but which show no significant structural conservation. but which show no significant structural conservation. But share 1 is characterised by six trateginal not structural structural manages to stransmembrane domains and intracellular and two intracellular loops. STRAP-2 exhibits a markedly different mRNA and two STRAP family members are differentially requilated. STRAP-1 expression is downregulated in some prostate cancers, whereas STRAP-1 expression is downregulated in some prostate cancers, strapper concerns and proteins is not capped and special stransmembrane concerns and proteins from the presence of six transmembrane concerns and proteins from the presence of six transmembrane concerns and pumporal immuno responses against stransmembrane specific antibodies. The antipodies may be used for detection; prognosis, and monitoring of cancers (or susceptibility to cancer), as therapeutic contains and protein proteins and be seed to their site of action. STRAP concerns and monitoring of cancers (or susceptibility special protein proteins and because anticaned proteins and proteins and because of the structure of action. STRAP concerns and monitoring of cancers (or susceptibility approtein proteins and because the protein proteins and proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gacttttacaaaattcctatagagattgtgaataaaaccttacctatagttgccattäct 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel proteins useful as diagnostic markers and therapeutic targets,
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                                                                                                                                                                                                                                                                       Saffran
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Pred. No. 5.3e-218;
0; Mismatches 1;
                                                                                                                                                                                                                                                                           Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             particularly for prostatic cancer
                                                                                                                                                                                                                                                                       Leong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Fig 9; 83pp; English.
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99.8%;
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Best Local Similarity 99.8
Matches 493; Conservative
UROGENESYS INC
                                                                                                                                                                                                                                                                           Hubert RS,
                                                                                                                                                     RAITANO A B.
SAFFRAN D C.
                                                                                                                                                                                                                                                                                                                                               WPI; 2000-072832/06.
                                    AFAR D E.
HUBERT R S.
                                                                                                                     LEONG K.
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Human ORF2 of Six-Transmembrane Protein of Prostate 1, STMP1.

(first entry)

BP.

AAS15810 standard; cDNA; 2238

AAS15810

AAS15810;

1416 t 1416

21 Sat Sep

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testis-specific polypeptides and the nucleic acids encoding them.
Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the proteins, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign of the testis or prostate particularly prostate cancer, benign cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancrealic cancer, liver cancer and lung cancer. The present sequence encodes prostate specific protein, Six-Transmembrane protein of Prostate 1, STMPI, ORF2.
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                                                                                          New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gatatttgtttctcaacatggcttatcagcaggttcatgcaaatattgaaaactcttgga 1235
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                                                                                                                                                                                        invention relates to substantially pure prostate-specific or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1561 BP; 420 A; 319 C; 346 G; 476 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 490; DB 22;
Pred. No. 3.3e-242;
0; Mismatches 1;
                                                                                                                                                          Claim 4; Fig 4H; 114pp; English.
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99.8%;
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                                             2001-662926/76.
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Best Local Similarity
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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign or prostatic hyperplasia, acute prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be testis. Other proliferative disorders for which the modulators may be cancer include lymphona, leukaemia, melanoma, voarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence represents the second open reading frame of a prostate
                                                                                                                  Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lumphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ss; ORF2.
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Query Match

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Description	Human cDNA encodin	Human ORF2 of Six-	Human STRAP-2 part	Human six transmem	Human cDNA encodin	Human ORF of Six-T	Human cDNA encodin	Human prostate gro	Human foetal liver
SUMMARIES	AAS15811	AAS15810	AAZ49398	AAD07072	AAS15802	AAS15801	AAS15813	AAZ46296	ABA57377
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Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 444)
Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
Compositions and methods for therapy and diagnosis of prostate
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Kalos,M.D. Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
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1 (Jases I to 250)

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,W.J.
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Direct, S. Sarten, S. C. Lander, E., Abraham, H., Allen, N., Bairen, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Bairen, B., Linton, L., Barna, N., Beckerly, R., Beda, F., Baddwin, C., Barna, N., Beckerly, R., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Collymore, A., Cooke, P., FitzHugh, M., Forrest, C., Gage, D., Galagan, J., Ferreira, P., FitzHugh, M., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Mardula, J., Lehoczky, J., Levines, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levines, R., Lieu, C., Liu, G., Locke, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnall, P., O'Donnall, P., O'Donnall, P., O'Donnall, P., O'Donnall, P., China, J., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pisani, C., Bollara, V., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACU21898 87401 bp DNA linear HTG 13-JUL-2000
Homo sapiens chromosome 15 clone RP11-407J8 map 15, LOW-PASS
SEQUENCE SAMPLING.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 87401)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone RP11-407J8
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                                                                                                                                            461
                                                                                                                                                                                                                                                                                     521
342 ttatcagcaggttcatgcaaatattgaaaactcttggaatgaggaagaagtttggagaat 401
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                                                                                                                                        208 TTATCAGCAGGTTCATGCAAATATTGAAAACTCTTGGAATGAGGAGAAGTTTGGAGAAT
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
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PAT 31-MAY-2001
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( bases 1 to 250)

Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Reed, S.G., Kalos, M.D., Retter, M.W., Stolk, J.A., Day, C.H., Skeiky, Y.A. and Wang, A.

Compositions and methods for the therapy and diagnosis of prostate
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                               342 ttatcagcaggttcatgcaaatattgaaaactcttggaatgaggaagaagtttggagaat 401
                                                                                                                                462 ttctatcccttcagtgagcaatgctttaaactggagagagttcagttttattcagtctac 521
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Pred. No. 3.8e-62;
0; Mismatches 1;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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illarity 99.5%;
Conservative
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Best Local Similarity
Matches 182; Conserv
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DEFINITION
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AX140723/c
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ORIGIN
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AX200583/c
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AUTHORS
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VERSION
KEYWORDS
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KEYWORDS
SOURCE
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1 (bases 1 to 250)

Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.

Compositions and methods for therapy and diagnosis of prostate cancer
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4 8233: gap of unknown length
4 40378: contig of 31145 bp in length
9 40478: gap of unknown length
9 172915: contig of 132437 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 300 others
                                                                                                                                                                                                                                                                                                                                                                         29.8%; Score 167; DB 2; Length 17
100.0%; Pred. No. 8.6e-82;
Live 0; Mismatches 0; Indels
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                                                                                   /organism="Papio cynocephalus anubis"
/db_xref="taxon:9555"
/clone="RP41-167P22"
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Pred. No. 3.8e-62;
0; Mismatches 1;
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40479. .172915
/note="assembly_fragment"
31733 c 32277 g 56096 t
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CORIXA CORPORATION (US)
LOCATION/QUALIFIERS
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Sequence 213 from Patent W00125272.
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/note="assembly_fragment"
8234. .40378
/note="assembly_fragment
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/note="assembly_fragment
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/db_xref="taxon:9606"
1. .250
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53 c 42 g
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AX106432.1 GI:13922111
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Best Local Similarity 99.5%;
Matches 182; Conservative (
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ORIGIN
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VERSION
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AUTHORS
TITLE
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AC099742.1 GI:17017546
HTG; HTGS_PHASE1; HTGS_DRAFT.
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DEFINITION
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VERSION
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (Dases 1 to 322)
Afar,D.E., Hubert,R.S., Raitano,A.B., Saffran,D.C., Mitchell,S.C.,
Faris,M. and Jakobovits,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DD 121604 CCTTTGTCAGAGATGTGATTCATCCATATGCTAGAAACCAACAGAGTGACTTTTACAAAA 121545
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Patent: WO 0140276-A 11 07-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 34.1%; Score 191; DB 2; Best Local Similarity 99.6%; Pred. No. 3.5e-95; Matches 241; Conservative 0; Mismatches 1
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Pred. No. 1.4e-85;
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/note="assembly_fragment" 66293 . .92168 /note="assembly_fragment" 92269 . .122036 /note="assembly_fragment" 122137 . .162928 /note="assembly_fragment" 122137 /note="assembly_fragme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                  vector_side:right"
29878 c 30533 g 50485
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Sequence 11 from Patent W00140276.
AX155253
AX155253.1 GI:14536717
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/db_xref="taxon:9606"
70 c 62 q 106
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99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 224; Conservative
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                                misc_feature
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                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
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AX155253
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SOURCE
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ארט 172915 bp DNA linear HTG 20-NOV-2001
Paplo cynocephalus anubis clone RP41-167P22, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
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1 (bases 1 to 172915)

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Gupta, J., Haghighi, P.,
Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q.,
Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D.,
McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y.,
Stantipop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Malker, M.A., Wetherby, K.D., Wiggins, L.,
Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    olive baboon.
Papio cynocephalus anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (20-NOV-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
95 TGAATAAAACCTTACCTATAGTTGCCATTACTTTGCTCTCCCTAGTATACTTGCAGGTC 154
                                                                                                     ttotggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttggt 214
                                                                                                                                          Center project name: 157922

Center clone name: 157922

Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Asgembly program: Phrap; version 0.990319
Consensus quality: 171910 bases at least Q40
Consensus quality: 17236 bases at least Q20
Insert size: 130000; agarose-fp
Insert size: 172615; sum-of-contigs
Quality coverage: 12.58% in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2438: contig of 2438 bp in length 2538: gap of unknown length 8133: contig of 5595 bp in length
                                                                                                                                                                                                                                                   215 tggaaacctggttacagtgtagaaaacagcttggattactaagtt 259
                                                                                                                                                                                                                                                                                        215 TGGAAACCTGGTTACAGTGTAGAAAACAGCTTGGATTACTAAGTT 259
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Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
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Sat

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Athter, N., Ayele, K., Beckstrom-Sternberg, S.W., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Lee, T. Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-G., Legaspi, R., Maduro, O.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 162928)
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-DEC-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 161001 bases at least Q40
Consensus quality: 161422 bases at least Q20
Insert size: 143000; agarose-fp
Insert size: 162428; sum-of-contigs
Quality coverage: 10.76x in Q20 bases; agarose-fp
Quality coverage: 9.47x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13922: contig of 13922 bp in length 14022: gap of unknown length 36248: contig of 22226 bp in length 66192: contig of 29844 bp in length 66292: gap of unknown length 92168: contig of 28876 bp in length 92268: gap of unknown length 122006: contig of 29768 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 25876 bp in length gap of unknown length contig of 29768 bp in length contig of 40792 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ Genome Center
Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                              NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
------ Project Information

    162928
    /organism="Pan troglodytes"
/db_xref="taxon:9598"
    /clone="RP43-120K11"

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36349. .66192
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1. .13922
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: ces
Center clone name: 120K11
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14023. .36248
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                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                       Pan troglodytes
                                                                                                                                                                                                                                                                                                           Unpublished
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36249
36193
66293
92169
122037
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                       ORGANISM
                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
                                                                                    REFERENCE
                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                       REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (sites)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
                                                                                                                                                                                                                                                                                          PAT 26-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compositions and methods for the therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 TTGTTTCTCAACATGGCTTATCAGCAGGTTCATGCAAATATTGAAAACTCTTGGAATGAG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 ttcgctatggtccatgttgcctacagcctctgcttaccgatgagaaggtcagagatat 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 gaagaagtttggagaattgaaatgtatatctcctttggcataatgagccttggcttactt 444
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                                                                               105 TCCCTCCTGGCAGTCACTTCTATCCCTTCAGTGAGCAATGCTTTAAACTGGAGAGAATTC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 ttgtttctcaacatggcttatcagcaggttcatgcaaatattgaaaactcttggaatgag 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162928 bp DNA linear HTG 12-DE Pan troglodytes clone RP43-120K11, WORKING DRAFT SEQUENCE, 6 UNDOTAGETED PIECES.
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Pred. No. 3.4e-101;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                            DNA
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/db_xref="taxon:9606"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Catarrhini; Hominidae; Homo.

Ku,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skeiky,Y.A. and Wang,A.

Compositions and methods for the therapy and diagnosis of prostate
                                              PAT 30-APR-2001
                                                                                                                                Euteleostomi;
                                                                                                                                                               Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A. Compositions and methods for therapy and diagnosis of prostate cancer
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Catarrhini; Hominidae; Homo.
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Matches 252; Conservative 0; Mismatches 1;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                             Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
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1 (bases 1 to 366)

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Sted,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J. Compositions and methods for the therapy and diagnosis of prostate
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Best Local Similarity 99.6%; Pred. No. 3.4e-101;
Matches 252; Conservative 0; Mismatches 1;
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Pred. No. 3.4e-101;
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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3774	amily="PTR .40125	/rpt_family="ALU" 4012640157	.4170	.4193	/rpt_family="L1" 4234842409	/rpt_family="ALU" complement(4294242982	.4442	/IPC_Idmily	4542245448	/rpt_ramily="Li" complement(4561545669	/rpt_ramily="Li" complement(45672, .45963	complement(4596446597	/*FC_raming	4837048785	/rpt_tamily="L1" complement(4957750216	complement(5054050791	complement(50820, .50985	/ipt_lamily="inf" complement(5112451156	/rpt_ramily="Li" 51405. 51691 /mt fom:1:-"htm"	complement(5172151764	/rpt_ramily="Li" complement(51765, .52058	/rpt_ramlly="ALU" complement(5225252467	Similarity 99.7%; Pred. No. 1. 3; Conservative 0; Mismatche	Jagatgtgattcatccatatgctaga			GATTGTGAATAAAACCTTACCTATA	aggtettetggeagetgettateaa	AGGICTICTGGCAGCTGCTTATCAA	ttggttggaaacctggttacagtgt	TTGGTTGGAAACCTGGTTACAGTGT	tatggtccatgttgcctacagcctc	TATGGTCCATGTTGCCTACAGCCTC	gatatttgtttctcaacatggcttatcagcaggt
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human BAC clone RG016J04 from 7q21, complete sequence.
AC002064
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                                                                                                                                                                                                                                                                               Score 439; DB 6; Length 24
Pred. No. 2e-233;
0; Mismatches 2; Indels
/note="unnamed protein product"
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11 Similarity 99.6%;
539; Conservative
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send an E-mail to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 9788x. For references see: Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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Actual start of this clone is at base position 1 of H_RG016J04;
actual end is at 156214 of H_RG016J04. The orientation of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone contains STS SWSS2784 (NID:g1113580) and SWSS893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                otherwise
                                                                                                                      Waterston, R.
Direct Submission
Submitted (09-MAY-1997)
Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, Mo 63108, USA
http://genome.wustl.edu/gsc
e-mail: sapiens@watson.wustl.edu
                                                 H. sapiens BAC clone RG016J04
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complement(9406. .9975)

/rpt_family="L1"

complement(10000. .11285)

/rpt_family="L1"
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15. 40
//rpt_family="L1"
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/organism="Homo sapiens"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 neighboring submissions.
1 (bases 1 to 156214)
Gattung, S. and Maggi, L.
The sequence of H. sapi
Unpublished (1997)
                                                                                                     (bases 1 to 156214)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAPPING INFORMATION:
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Perfect score:

Sequence:

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Run on:

Scoring table:

Word size :

Searched:

Minimum DB Maximum DB

Database :

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PAT 22-JUN-2001
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AC005548 Homo sapi
AL133173 Human DNA
AL45993 Homo sapi
AC015921 Homo sapi
AC01591842 Homo sapi
AC002449 Human PAC
U64836 Caenorhabdi
U2944 Caenorhabdi
AC105037 Homo sapi
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1 (bases 1 to 2453)
Afar, D.E., Hubert, R.S., Raitano, A.B., Saffran, D.C., Mitchell, S.C., Faris, M. and Jakobovits, A. Serpentine transmembrane antigens expressed in human prostate cancers and uses thereof
Patent: WO 0140276-A 7 07-JUN-2001; Urogenesys, Inc. (US)
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AC034151
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AC092404
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AX155249
AX155249.1 GI:14536713
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355. .1719
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AX155253
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AX267239
AC021898
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     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                             residues
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                                                    September 20, 2002, 09:53:50
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                                                                                                                                                                                                                    Post-processing: Listing first 45 summaries
                                     - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Score

Result

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760 bp DNA linear GSS 08-MAR-2000 nbeb0051M09f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic AZ045243
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/db_xref="taxon:4530"
/dlone="OSCNBB0051M09f"
/clone=lib="CuGI Rice BAC Library (EcoRI)"
/tlssue_type="Leaf"
/lab_host="E. coli DH10B"
/lab_host="E. coli DH10B"
/lab_host="E. coli DH10B"
/lab_host important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18 432 clones (doubly spotted), represent the whole library for colony excreening and can be requested from the Clemson University
                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 760)
Wing, R.A. and Dean, R.A.

A BAG End Sequencing Framework to Sequence the Rice Genome
Contact: Wing RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n-24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Wipponbare variety using EcoRI as the cloning enzyme. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 5.0%; Score 20; DB 12; Length 760; Best Local Similarity 100.0%; Pred. No. 43; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence start: 31
High quality sequence stop: 304.
Location/Qualifiers
1..760
/organism="Oryza sativa"
/strain="Japonica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Seq primer: GTAAAACGACGCCAGTG
Class: BAC ends
                                                                                                                                                                       A2045243.1 GI:7206979
                                                                                                                                                                                                                               Oryza sativa.
                                                                                                                                                                                                                                                               sativa
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Gaps

.; 0

82 ggtttatatatgcagcaaca 101

ò qq

Search completed: September 20, 2002, 08:33:47 Job time: 8711 sec

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Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55.296 clones with an average insert size of 121 Kb providing approximatiey 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18 432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BACAETR Resource Center (www.genome.clemson.edu)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 566)
Mahairas, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS 27-AUG-1999
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84 c c 73 g 215 t 11 others
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University of Mashington
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: juallacedu washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from che human BAC library RPCI-11. For BAC
Clones are derived from che human BAC library RPCI-11. For BAC
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Clones are derived from the human BAC library RPCI-11. For BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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/clone="Plate=1097 Col=8 Row=A"
/clone_lib="RPCI-11 Human Male BAC Library"
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45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20; DB 100.0%; Pred. No. 45; Live 0; Mismatches
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Location/Qualifiers
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Plate: 1097 row: A column: 8
Seq primer: T7
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AQ831336.1 GI:5797398
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AL (Dases 1 to 741)

RS Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPC1-23

AL Uppublished (1999)

Other_GSS: RPC1-23-335ES.TJ

Contact: Shaying Zhao
Cheart: Shaying Zhao
Chart. Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Eax: 301 838 0200
Eax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPC1-23. For BAC
Llones are derived from the mouse BAC library availability, please contact Pleter de Jong
(pieteredejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://worcpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 335 row: E column: 5
Geg primer: T
                                                                                                                                                                                                         RPCI-23-335E5.TV RPCI-23 Mus musculus genomic clone RPCI-23-335E5, AZ019656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoR1: Site_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECOR1 sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

150 c 124 g 230 t 1 others
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 721)
                                             Gaps
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DB 12; Length 566; 45;
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/strain="C57BL/6J"
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100.0%; Pred. No.
:ive 0; Mismatch
5.0%; Score 20;
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/clone="RPCI-23-335E5"
/clone_lib="RPCI-23"
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/lab_host="DH10B"
  5.00,
100.0%; Pre-
                                                                                   247 tataagcttggccacatttt 266
                                                                                                          206 TATAAGCTTGGCCACATTT 225
                                                                                                                                                                                                                                                                                                                           AZ019656.1 GI:7095040
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                    Best Local Similarity 100.
Matches 20; Conservative
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AUTHORS
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Hilllart,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkln,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
                                                                                                                                                                                                                         /clone="InAGE:4450328"
/clone=lib=NIH_MGC_90"
/tissue_type="adenocarcinoma, cell line"
/tab.host="DH10B (phage-resistant)"
/ab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pcNV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
/Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

a 154 c 172 g 267 trary."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
Insert Size: 1499
High quality sequence stops: 253 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1499 Std Error: 0.00
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can holden distribution: MGC clone distribution information in thitp://image.lln.gov
http://image.lln.gov
http://image.lln.gov
laddings.rolln.gov
loguality sequence stop: 639.
Location/Qualifiers
1.838
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:470661"
/db_xref="taxon:9606"
/clone="IMAGE:115044"
/sex="male"
/dev_stage="20 week-post conception fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 10; Length 838;
Pred. No. 14;
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100.0%; Pred. No. 14;
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Seq primer: M13RP1
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Best Local Similarity 100.
Matches 21; Conservative
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Fax: 314 286 1810
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Aice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n-24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Barle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ912082 512 bp DNA linear GSS 02-DEC-1999 nbeb0016A11f CUGI Rice BAC Library (ECORI) Oryza sativa genomic clone nbeb0016A11f, DNA sequence.
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Divaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 512)
Wing,R.A. and Dean,R.A.
A BAC Sequencing Framework to Sequence the Rice Genome
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                                                                                                                                                                                                                                                                           Score 20; DB 10; Length 488; Pred. No. 46; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contect: Wing RA Clemson University Genomics Institute Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
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High quality sequence stop: 407.
Location/Qualifiers
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AQ912082.1 GI:6508598
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninol.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="6030497E09"
/clone_lib="RIKEN full-length enriched, 13 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="testis"
/dev_stage="13 days embryo"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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BE039135 756 bp mRNA linear EST 07-JUN-2000 AB14A10 AB Arabidopsis thaliana cDNA 5' similar to homogentisate 1:
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Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Eunctional Genomics of Plant Stress Tolerance
Unpublished (2000)
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                                                                                                                                                                                     Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Michalowski,C.B.
Contact: Michalowski,C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: S20-621-7982
Fax: 520-621-1697
Email: cDm@u.arizona.edu
Insert Length: 1 Std Error: 0.00.
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/cultivar="Columbia"
/db_xref="taxon:3702"
/clone_lib="AB"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/dev_stage="2-3 weeks"
/note="200mm NaCl"
                                                       -dioxygenase, mRNA sequence.
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Gaps ö

5.5%; Score 22; DB 9; Length 628; 100.0%; Pred. No. 4.7; O; Indels ive 0; Mismatches 0; Indels

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house mouse.
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                                                                                     /db_xref="taxon:1000"
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polylinker; Site_1: Not 1; Site_2: Eco R1; The
NIH_BMAP_M_S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hipoccampus) after a series of subtracted libraries
were generated in this process: NIH_BMAP_M_S4.
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
NIH_BMAP_M_S3.1 clones from which 3' ESTS had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.2,
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles (subtracted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           into DHIOB bacteria (Liferenhologies) to generated har DHIOB bacteria (Liferenhologies) to generate the NHL BMAP M.S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 5.791-806, 1996)
TAG_LIB=NIH_BMAP_M_S4
TAG_LIB=NIH_BMAP_M_S4
TAG_LISSUE-prineal-glands
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 712)
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Dunn,D., Aoyad,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Welss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                  /organism="Mus musculus"
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University of Utah Genome Center
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                                                                        /strain="C57BL/6J
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(http://www.fax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114)pblArL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into capators complementary to complementary to capators and selected for ampicillin resistance."
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 628)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,

Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda

M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,

Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasaki

D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tanaka,H.,

Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,

Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB621516 RIKEN full-length enriched, 13 days embryo male testis Musmusculus cDNA clone 6030497E09 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
//lab.host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="UUGC1M0212F14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.7%; Score 23; DB 12; Length 712;
100.0%; Pred. No. 1.5;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                              Std Error: 0.00 column: 14
                                                                                                                                                                                                                                 Insert Length: 10000 Std Error: Plate: 0212 row: F column: 14 Seq primer: CGTFGTAAAACGACGGCCAGT Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 712.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
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Query Match 7.9%
Best Local Similarity 100.0
Matches 32; Conservative
                    Tel: 402 762 4366
Fax: 402 762 4390
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Fax: 301 443 9890
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                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: capaba-refamil.nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 1000 Std Error: 0.00
Seq primmer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pAMP10; mRNA made from prostatic intraepithelial neoplasia (low-grade), CDNA made by oligo-dr priming. Non-directionally cloned. Size-selected on agarcse gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
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                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 322) NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine (Unpublished (2000)) CONTECT: Smith TPL USDA, ARS, US Meat Animal Research Center
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384188 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BI359597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Pr6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="prostate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:941693"
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56:5380-5383."
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                    AA508880.1 GI:2245821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                              Tumor Gene Index
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                                                                            Homo sapiens
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Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the pineal glands tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
                                                                            Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 136 cg 188 t
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UI-M-BH3-brx-g-01-0-UI.sl NIH_BMAP_M_S4 Mus musculus cDNA clone
UI-M-BH3-brx-g-01-0-UI 3', mRNA sequence.
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 595;
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Pred. No. 6.5e-05;
Clay Center, NE 68933-0166,
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100.0%; Pred. No. v.
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="MARC 2PIG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Sus scrofa"
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                                                                                                                                                                                                                                                                                BACKWARD: GTTTTCCCAGTCACGACG
Plate: 132 row: H column: 3
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                 FORWARD: AGGAAACAGCTATGACCAT
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Tumor Gene Index
Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Email: capaba-refmail.nih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA.Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M. A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham.
           /dev_stage="Adult"
/dev_stage="Adult"
/dev_stage="Adult"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: lung_tumor; Vector: pucl8; Site_1: SmaI;
/note="Organ: lung_tumor; Vector: pucl8; Site_1: SmaI;
/note="Organ: lung_tumor; Vector: pucl8; Site_1: SmaI;
/note_1: SmaI; A mini-library was made by cloning products
/derived from Organs; Destricts Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the Pucl 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                            32.0%; Score 129; DB 10; Length 483; 100.0%; Pred. No. 5e-52; Live 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
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Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs remail.nih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Tissue Procurement: W. Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: N.T.-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40n13 fwd. Efrom Amersham.
                                                                                                                                                                                                                                                                      AA935972 181 bp mRNA linear EST 28-APR-1998 ny30h06.sl NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1273307,
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information can be
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ng86f03.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:941693, mRNA
sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 181)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                         Length 181;
            Length 180;
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Pred. No. 1.5e-14;
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100.0%; Pred. No. 1...
... 0; Mismatches
12.9%; bccd. No. 100.0%; Pred. No. 100.0%; pred. No. 100.0%; Mismatches
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/db_xref="taxon:9606"
/clone="InhaGE:1273307"
/clone_lih="NCI_CGAP_Pr12"
/sex="male"
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52; Conservative
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Best Local Similarity 100.
Matches 52; Conservative
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September 20, 2002, 08:33:44 ; Search time 5053.42 Seconds
(without alignments)
1076.355 Million cell updates/sec
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403
1 cccagattctttgattgtca......ctttgctccccctagtatac 403
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                           OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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em_gss_hum:* em_gss_inv:* em_gss_pln:* em_gss_vrt:* em_estin: * em_estwu: * em_estp: * em_estro: * em_htc: * gb_est1: * gb_htc: * gb_htc: * gb_htc: * 10: 12: 13:

summaries

Post-processing: Listing first 45

em_estba:* em_esthum:*

EST:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BF883142 QV3-ET021	AA888667 nw77b11.s	AA935972 ny30h06.s	AA508880 nq86f03.s	BI359597 384188 MA	BI133492 UI-M-BH3-	AZ428664 1M0212F14	BB621516 BB621516	BE039135 AB14A10 A	BG119803 602352138	T87479 yd85e07.rl	AQ912082 nbeb0016A	AQ831336 HS_5521_A	AZ019656 RPCI-23-3	AZ045243 nbeb0051M	AG165588 Pan trogl	AQ248591 T5K8-T7 T	
SUMMARIES	ΩI	BF883142	AA888667	AA935972	AA508880	BI359597	BI133492	AZ428664	BB621516	BE039135	BG119803	T87479	AQ912082	AQ831336	AZ019656	AZ045243	AG165588	AQ248591	
	DB	10	σ	6	6	10	10	12	6	6	10	10	12	12	12	12	12	12	
	Query Match Length DB	483	180	181	322	595	561	712	628	756	838	488	512	999	721	760	803	109	
æ	Query	32.0	12.9	12.9	12.4	7.9	6.5	5.7	5.5	5.2	5.2	5.0	5.0	5.0	5.0	5.0	5.0	4.7	
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A1305509 qw72al0.x AV2264258 AV264258 AU077687 AU077687 BF085019 QV1-MT016 BF085019 QV1-MT016 BF085019 QV1-MT016 BF085019 QV1-MT016 BF085019 GV1-MT016 BF085019 GV1-MT016 BF085019 GV1-MT016 BF085019 GV1-MT016 BF085019 GV1-MT016 BF085019 GV1-MT018 BF085019 GV1-MT018 BF085019 GV1-MT018 BF085019 GV1-MT019 BF085019 GV1-M	HERBRIAL2 BERBRIAL2 ON 073-EF0211-071200-529-D10 ET0211 Homo sapiens CDNA, mRNA sequence. BFBRIAL2 NO 073-EF0211-071200-529-D10 ET0211 Homo sapiens CDNA, mRNA sequence. BFBRIAL2.1 GI:12273268 EST. House and the sequence of correals. Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Dias Neto.E. Cadacia Correal, R., Verjovski-Almeida, S., Binones, M.R., Nagai, M.A., Garcia Correal, R., Verjovski-Almeida, S., Einposon, D.H., Brunstein, A., daoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J. Brunstein, A., daoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J. Shotgun sequence tags Sequence tags Sequence tags Sequence tags Contact Simpson A.J.G. Laboratory of Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil. Fel: 1-55-11-2707001 Email: asimpson@ludwig.org.br/ Project This antry can be seen in the FARESP/LICR Human Cancer Genome Project This antry can be seen in the following UBL Froject This antry can be seen in the following UBL Froject This antry can be seen in the following UBL Froject This antry can be seen in the following UBL Froject This antry sequence start: 26 High quality sequence stop: 433. Location(Outlifiers Location(Outlifiers) Location(Outlifiers) Location(Outlifiers) Location(Outlifiers)
AL305509 AL223600 AV264258 AU077687 BER95019 BG019784 P95226 AA701826 BI350635 AQ647805 AQ647805 BM034788 BH454179 BH454179 BH65789 BM035184 AZ179970 AZ179933 BI864138 BI864138 BI864138 BIR6789 AW305417 AZ371568 AZ371568 AZ371568 AZ371568 AZ371568 AZ371568 AZ371568 AZ371568	ALIGNMENT: 483 bp 9-bl0 ET0211 268 Chordata; Crai Primates; Cati Correa,R., V ,W. JI., Zago ho,A.F., Matsi entani,R.R., f the human t. i. U.S.A. 97 i. U.S.A.
210 9 214 9 2210 9 2214 9 2341 10 2361 10 2361 10 2362 10 2362 10 2363 10	BF883142 BF883142 Ov3-ET0211-071200-529-b10 ET0211 HB883142 BF883142.1 GI:12273268 EST. Home sapiens Eukaryota; Metazoa; Chordata; Cran; Mammalia; Eutheria; Primates; Cata; Home sapiens Eukaryota; Metazoa; Chordata; Cran; Mammalia; Eutheria; Primates; Cata; I bases 1 to 48; Dias Neto,E., Garcia Correa,R., Ve; Nagai,M.A., da Silva,W. Jr., Zago, Goldman,G.H., Carvalho,A.F., Matsul Brunstein,A., deOliveira,P.S., Buc, M.J., Soares,F., Brentani,R.R., R. Simpson,A.J. Shopton sequencing of the human tra Sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7) Contact: Simpson A.J.G. Ludwig Institute for Cancer Researt Rua Prof. Antonio Prudente 109, 4 in the 1+55-11-2707001 Email: asimpson@ludwig.org.br FAX: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the Project. This entry can be seen in (http://www.ludwig.org.br/Scripts/(071200-529-b10643-2000-12-07844=1) Encation/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Outlifiers Location/Outlifiers Location/Outlifiers Location/Outlifiers Location/Outlifiers Location/Outlifiers Location/Outlifiers Location/Outlifiers Location/Outlifiers
000000000000000000000000000000000000000	BF883142 QV3-ET0211- BF883142 BF883142.1 EST. Home sapier Eukaryota; Home sapier Eukaryota; Home sapier Eukaryota; Home sapier Eukaryota; Home sapier Brunstein, A., M.J., Soal Simpson, A., Simpson, A., Simpson, A., Simpson, A., Simpson, A., Simpson, A., Eudali, Simpson, A., Simpson, A., Simpson, A., Simpson, A., Simpson, A., Simpson, A., Frontani, Simpson, A., Simpso
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 BER83142/C LOCUS DEFINITION ACCESSION VERYWORDS SOURCE ORGANISM AUTHORS AUTHORS TITLE JOURNAL MEDLINE COMMENT FEATURES SOURCE SOURCE SOURCE

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Sequence 6, Application US/08789329C

Patent No. 6165755

GENERAL INFORMATION:
TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
TITLE OF INVENTION: LLP
STREET: OF WORLD Trade Center
STREET: ONE WORLD TRADE CONTENT: United States of America
COUNTRY: United States of America
STRATE: Oregon
COUNTRY: United States
COUNTRY: United States
STRATE: OREGON
COUNTRY: United States
STRANBENGE WORLD NATA:
APPLICATION NUMBER: US/08/789,329C
FILING DATE: UNIVER: 2847-46468/DJE
TELEPAN: (503) 226-7391
TELEPHONE: (503) 226-7391
TELEPAN: (503) 226-7391
US-08-789-329C-6
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ó Gaps ó; 4.0%; Score 16; DB 4; Length 1079; 100.0%; Pred. No. 37; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 16; Conservative ò

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Search completed: September 20, 2002, 09:51:09 Job time: 11857 sec

Gaps

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                                                                                                                                                   Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL TITLE OF INVENTION: FOR IMPROVED POULTRY PRODUCTION NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSE: Whinston, LLP STREET: One World Trade Center STREET: 121 S W. Salmon Street STREET: Suite 1600 CITY: Portland CITY: Portland CITY: Portland
                                                                                                                                                                                           .
0
                                                                                                                                                DB 2;
37;
                                                                                                                                                Query Match 4.0%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 37; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Uregon
COUNTRY: United States of America
ZIP: 97204-2988
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFRATING SYSTEM: Windows NT
SOFRATING SYSTEM: Windows NT
SOFRATING SYSTEM: UNIONBRE: US/08/789,329C
FILING DATE: 01/23/97
CLASSIFICATION NUMBER: US/08/789,329C
FILING DATE: TASSIFICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: EARLY DAVIG A
REDISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 2847-46468/I
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08789329C Patent No. 6165755 GENERAL INFORMATION:
; TYPE: nucleic acid
; STRANDENNESS: double
TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-832-877-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    627 TAAAACCTTACCTATA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 16; Conserve
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Patent No. 5840506
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C. STREET: Suite 1800 Two Penn Center Plaza CITY: Philadelphia STATE: PA A A A COUNTRY: USA ZIP: 19102
                               ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.0%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 37; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                        8321-13 US1
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                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,480
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321
TELECOMMUNICATION INPORMATION:
TELEFAX: (215) 568-5849
INPORMATION FOR SEQ ID NO: 56: SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYRE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-
TELECOMMUNICATION INFORMATION:
TELEFRAME (215) 568-8383
TELEFAX: (215) 568-559
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-832-883-56
                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          627 TAAAACCTTACCTATA 612
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                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-08-832-877-56/c
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RESULT 12
US-08-132-813-56/C
US-08-132-813-56/C
Sequence 56, Application US/08832883
Patent No. 5807681
GENERAL INFORMATION:
APPLICANT: Glordano, Antonio
APPLICANT: Baldi, Alphonso
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS;
TORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SETIDEL, GONDA, LAVORGNA & MONACO, P.C.
STREET: Suite 1800 TWO Penn Center Plaza
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 203;
                                                                             APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Cornish, Edwina C.
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
TITLE OF INVENTION: 29
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE PATENTIAN STATES OF THE SOFTWARE SOFTWARE PATENTIAN DATA:
APPLICATION NUMBER: US/08/502,046
FILING DATE: 14-JUL-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/285,309
FILING DATE: 03-AUG-1994
ATTORNEY/AGBRY INFORMATION:
NAME: D16141io, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/POCKET NUMBER: 86332
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
38;
                                                                                                                                                                                                                               ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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100.0%; Pred. No.
live 0; Mismatc
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                 Sequence 27, Application US/08502046 Patent No. 5861487 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: DNA (genomic) US-08-502-046-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEFX: 230 901 SAS UR
INFORMATION FOR SEQ ID NO: 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 203 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ATCAGCCAGAGAGATT 136
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Best Local Similarity 100.
Matches 16; Conservative
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ADDRESSEE: Scully, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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: U.S.A.
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                              11530
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COUNTRY:
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     Gaps
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                                                                                                                                         APPLICANT: HOLLON, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Tanaka, Yoshikazu
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.0%; Score 16; DB 1; Length 203; 100.0%; Pred. No. 38;
   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City Plaza STATE: New York COUNTRY: U.S.A. ZIP: 11530
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 Mismatches
                                                                                                                                              Sequence 35, Application US/08313075A Patent No. 5639870
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                              203 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 atcagccagagagatt 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ATCAGCCAGAGAGATT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 4.0
Best Local Similarity 100.
Matches 16; Conservative
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
US-08-313-075A-35
                                                                                                                              US-08-313-075A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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 Matches
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GENERAL INFORMATION:
APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
TITLE OF INVENTION: GENETIC SEQUENCES COURSESPONDENCE ADDRESSE: SUlly, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 203; 38;
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38;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/285,309
FILING DATE: 03-40G-1994
FILING DATE: 03-40G-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Diciglio, Frank S.

REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 86332
FELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFERS: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                        Query Match 4.0%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 38; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.0%; Score 16; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Application US/08285309 Patent No. 5569832
                                 ** CELEPAN: (516) 742-4343

** TELERA: (516) 742-4343

** TELEX: 230 901 SANS UR

** INFORMATION FOR SEQ ID NO: 27:

** SEQUENCE CHARACTERISTICS:

** LENGTH: 203 base pairs

** TYPE: NUCLEIC ACID

** STRANDEDNESS: single

** TOPOLOGY: linear

** MOLECHIP*** TOPOLOGY: linear
                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) US-07-912-900-27
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              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 203 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 atcagccagagagatt 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ATCAGCCAGAGATT 136
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Patent No. 5349125

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Holton, Timothy A.

APPLICANT: Cornish, Edwina C.

APPLICANT: Tanaka, Yoshikazu

APPLICANT: Lester, Diane R.

TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID

TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.0%; Score 16; DB 1; Length 180;
100.0%; Pred. No. 38;
.ive 0; Mismatches 0; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,075A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/912,900
FILING DATE: 19920713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                               PULGATION DATA:
APPLICATION NUMBER: AU PL 1538/92
PEILING DATE: 27 - MAR-1992
PEILING DATE: 27 - MAR-1992
PEILING APPLICATION DATA:
APPLICATION NUMBER: AU PL 6698/93
FELING DATE: 07 - JAN-1993
PFLING DATE: 07 - JAN-1993
PFLING DATE: 07 - JAN-1993
PFLING DATE: 25 - MAR-1993
APPLICATION NUMBER: AU PCT/AU93/00127
APPLICATION NUMBER: AU PCT/AU93/00127
APTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, FRANK S.
REGISTRATION NUMBER: 9433
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHANE: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION POR SEG ID NO: 40:
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. ....ек: US/08/313,075A
. ... 30-NOV-1994
. ON: 800
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NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 180 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 atcagccagagatt 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 ATCAGCCAGAGAGATT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garden City
: New York .
RY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                             FILING DATE: 3(CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: 11:
; MOLECULE TYPE:
US-08-313-075A-40
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US-07-912-900-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Gaps

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APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERRENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.160SU2
CURRENT APPLICATION NUMBER: 05/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1999-06-30
                                                                                                                                                                                         342 ctatagagattgtgaataaaaccttacctatagttgccattactttgctc 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENETIC SEQUENCES ENCODING FLAVON PATHWAY ENZYMES AND USES THEREFOR
                                                                                Score 50; DB 4; L
Pred. No. 9.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.4%; Score 50; DB 4; L 100.0%; Pred. No. 9.6e-17; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                               NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 40, Application US/08313075A; Patent No. 5639870; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09323873A Patent No. 6329503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Holton, Timothy A. APPLICANT: Cornish, Edwina C. APPLICANT: Tanaka, Yoshikazu
                                                                                                                         50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.4
Best Local Similarity 100.
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: ADDRESSE: Scully, S
; ORGANISM: Homo Sapiens
US-09-323-873A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo Sapiens
US-09-323-873A-7
                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 400 Garde CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-313-075A-40
                                                                                                                                                                                                                                                                                        US-09-323-873A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                         Matches
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GENERAL INCRMATION:
GENERAL INCRMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: APPLICANT: Novel SERVENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERVENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.16USU2
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/097,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR PLING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 328,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.0%; Score 153; DB 4;
99.5%; Pred. No. 4.9e-70;
live 0; Mismatches 1
                                                                    APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Fanger, Gary
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE C
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 212
LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 322
TYPE: DNA
                   Harlocker, Susan Louise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 gagagattgaaaatttacccctac 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 gagagattgaaaatttacccctac 247
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                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature

LCCATION: (1)...(328)

CTHER INFORMATION: n = A,T,C or G

US-09-439-313-212
Mitcham, Jennifer L
                                                         Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 203; Conservative
                                        Jiang Yuqui
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-323-873A-9
                                        APPLICANT
                                                           APPLICANT
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278 ggtagctataagcttggccacattttttt 307
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                                                                                                       ggttattgaacttgcccgccagttgaatttcattcccattgacttgggatccttatcatc 180
                                                                  61 acctaaggatgccagccggcaggtttatatatgcagcaacaatattcaagcgcgacaaca 120
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              GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Matcham, Jennifer L.
APPLICANT: Realock. Susan Louise
APPLICANT: Realock Steven G.
APPLICANT: Realock Steven G.
APPLICANT: Realock Mark
APPLICANT: Retter, Mark
APPLICANT: Retter, Mark
APPLICANT: Retter, Mark
APPLICANT: Caig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: OMPOSITION SOF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastsEQ for Mindows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Pred. No. 3.5e-104;
0; Mismatches 1; Indels
                                                                                                                                                            ggtagctataagcttggccacattttttt 270
                                                                                                                                                                                                                                                      Sequence 214, Application US/09439313
Patent No. 6329505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature

LCCATION: (1)...(444)

CTHER INFORMATION: n = A,T,C or G

US-09-439-313-214
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99.6%;
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Best Local Similarity 99.6
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapten
                                                                                                                                                                                                                                            US-09-439-313-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEO ID NO 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PE: DNA
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APPLICANT: XX, Jiangchun
APPLICANT: XX, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 aggatgccagccggcaggtttatatatgcagcaacaatattcaagcgcgacaacaggtta 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 ttgaacttgcccgccagttgaatttcattcccattgacttgggatccttatcatcagcca 185
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                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 153; DB 4;
Pred. No. 4.9e-70;
0; Mismatches 1
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Patent No. 6229505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
Sequence 212, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 gagagattgaaaatttacccctac 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SED ID NO: 212:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 BASE pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 38.0%;
Best Local Similarity 99.5%;
Matches 203; Conservative (
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US-09-030-607-212
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CLASSIFICATION:
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US-09-030-607-214
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTufS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTufS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-323-873A-9
US-09-323-873A-9
US-08-313-075A-40
US-08-313-075A-40
US-08-313-075A-35
US-08-313-075A-35
US-08-313-075A-35
US-08-832-883-56
US-08-832-883-56
US-08-789-329C-9
US-08-789-329C-9
US-08-789-329C-2
US-08-465-794-5
US-08-465-794-5
US-08-465-794-5
US-08-663-191A-2
US-08-117-491-25
US-08-117-491-25
US-08-117-491-25
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                                                                              nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
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Match Length
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Maximum DB
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Sequence 214, Application US/09030607

Patent No. 6262245

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 3.5e-104;
; Mismatches 1; Indels
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APPLICATION NUMBER: US/09/030,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
US-08-789-329C-1
US-08-755-587-15
US-08-099-753-3
US-09-099-753-3
US-08-639-501-1
US-09-044-946-1
US-09-044-908-1
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US-09-128-135-13
US-09-128-155-17\/
US-08-133-124A-1070
US-08-373-124A-1070
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NAME: Maki, David J.
REGISTATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                             Novel polynucleotide encoding polypeptide comprising a portion of prostate tumour protein useful for inhibiting development of prostate cancer or for treating prostate cancer in a patient
                                                                                                                                ggttattgaacttgcccgccagttgaatttcattcccattgacttgggatccttatcatc 180
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                                                                Gaps
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                                             Length 444;
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                  G; 143 T; 3 other;
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                                            Score 219; DB 22;
Pred. No. 2.1e-104;
0; Mismatches 1;
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                  Sequence 444 BP; 120 A; 100 C; 78
polynucleotide of the invention.
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97US-0904804.
98US-0020956.
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                                            tch 54.3%; al Similarity 99.6%; 269; Conservative
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01-AUG-1997;
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                                            Query Match
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Matches 269
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Length 444;
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Score 219; DB 22;
Pred. No. 2.1e-104;
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llarity 99.6%;
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Query Match
Best Local Similarity
Matches 269; Conserv
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Search completed: September 20, 2002, 09:59:50 Job time: 11708 sec

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The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express the polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06541 to AAA06691 and AAA82000 to AAX82000 to Expresent sequences used in the exemplification of
                                                                                                                                                                                                                                         Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:214.
Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide useful for treating and diagnosing comprises an immunogenic portion of prostate tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu J,
                                                                          ggtagctataagcttggccacattttttt 307
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                                            ggtagctataagcttggccacatttttttt
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                                                                                                                                                    BP.
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980S-0159812.
980S-0159822.
990S-0232149.
990S-0232880.
                                                                                                                                                 AAA06447 standard; cDNA; 444
                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US15838
                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0115453
                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
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                                                                                                                                                                                                                                                                                                                                             WO200004149-A2.
                                                                                                                                                                                                                                                                                                                   Homo sapiens
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09-APR-1999;
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polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer - \,
180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kalos MD;
Carter D;
                                                                                                     ggttattgaacttgcccgccagttgaatttcattcccattgacttgggatccttatcatc
                                                                                                                                                                                                                                                                                                                                                  Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated prostate-specific
                                                                                                                                                        ggtagctataagcttggccacattttttt 270
                                                                                                                                                                      prostate cDNA sequence #207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 302; 579pp; English.
                                                                                                                                                                                                                                               BP.
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2000US-0605783.
2000US-0636215.
2000US-0651236.
2000US-0679426.
2000US-0685166.
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2000US-0570737
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12-MAY-2000;
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10-AUG-2000;
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Indels

DB 21; Length 444;

54.3%; Score 219; DB 21; 99.6%; Pred. No. 2.1e-104; ive 0; Mismatches 1;

Conservative

Query Match Best Local Similarity Matches 269; Conserv

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218 agccanagagattgaaaatttacccctacgactctttactctctggagagggccagtggt 277
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                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.
         262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 agccagagagattgaaaatttaccctacgactctttactctctggagagggccagtggt 240
                        121 cccctacgactctttactctctggagagggccagtggtggtagctataagcttggccaca 180
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         cccctacgactctttactctctggagagggccagtggtggtagctataagcttggccaca
                                                                                                                                                                                                                                                                                                                                                    portions of prostate proteins of prostate cancer
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                                                                                                                                                                          Prostate; cancer; tumour; vaccine; immunogen; clone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 444 BP; 120 A; 100 C; 78 G; 143 T; 3 other;
                                                                                                                                                        Forward DNA sequence of prostate tumour clone 8-b6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.3%; Score 219; DB 19;
99.6%; Pred. No. 2.1e-104;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                    Polypeptides comprising immunogenic used in a vaccine for the treatment
                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Page 121; 130pp; English.
                                                                                                                                                                                                                                                              98US-0020956.
97US-0806099.
97US-0904804.
                                                                                                     AAV61348 standard; cDNA; 444
                                                                                                                                                                                                                                              98WO-US03492
                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                  WPI; 1998-609886/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                  Xu J;
                                                                                                                                                                                                                                                              09-FEB-1998;
25-FEB-1997;
01-AUG-1997;
                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                            WO9837093-A2
                                                                                                                                                                                                                                              25-FEB-1998;
                                                                                                                                       06-JAN-1999
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                                                                                                                       AAV61348;
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Best Local S
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prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 acctaaggatgccagccagcaggtttatatatgcagcaacaatattcaagcgcgacaaca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggttattgaacttgcccgccagttgaatttcattcccattgacttgggatccttatcatc
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                                                                                                                                                                                                                                                                                                                      tumour specific gene; human; prostate cancer; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 219; DB 19;
Pred. No. 2.1e-104;
0; Mismatches 1;
                                                                                                                                                                                                                                                                               Prostate tumour specific gene clone 8-b6
Claim 1; Page 131; 141pp; English.
                                                                                                                                                  BP
                                                                                                                                                    standard; cDNA; 444
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97US-0806596.
97US-0904809.
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llarity 99.6%;
Conservative
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                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                               WO9837418-A2.
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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25-FEB-1997;
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                                                                                                                                                                                                                                  08-DEC-1998
                                                                                                                                                                                                                                                                                                                                              therapy; ss.
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Best Local Simi
Matches 269;
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                                                                                                                                               AAV58684
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181 ttttttttcctttattcctttgtcagagatgtgattcatccatatgctagaaa 233

RESULT

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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be
                                                                                                                                              Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                                                                                                                                  benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ds; exon 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence represents exon 4 of a prostate specific protein,
                                                                                                  Human Six-Transmembrane Protein of Prostate 1, STMP1, exon 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 528 BP; 139 A; 116 C; 102 G; 171 T; 0 other;
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                                                             16-JAN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                  WO200172962-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saatcloglu F;
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Length 528;
                                                                                                                                    Indels
                                                           Sequence 528 BP; 139 A; 116 C; 102 G; 171 T; 0 other;
                                                                                                       Score 233; DB 22;
Pred. No. 1e-111;
                                                                                                               100.0%; Pred. ....
                                                                                                        57.8%;
                                                                                                                      Best Local Similarity 100.
Matches 233; Conservative
                                spliced version, ORF2.
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                                Gaps
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57.8%; Score 233; DB 22; Length 528; 100.0%; Pred. No. 1e-111;
                               0; Indels
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100.0%; Pred. nc.

Best Local Similarity 100. Matches 233; Conservative

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203 121 263

Query Match

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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the protein, antibodies against the proteins. Compounds that modulate the prostating modulators of the roteins. Compounds that modulate the prostating modulators of the proteins of the testis or prostate particularly prostate cancer, benign of the testis or prostate particularly prostate cancer, benign or prostatic hyperplasia, acute prostatilis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, threat cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence represents econ 4 of a prostate specific protein, alternatively
                                                                                                                                                               Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                                                                                                                                                benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ds; exon 4; ORF2.
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AAS15806 standard; DNA; 528
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                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SAAT/) SAATCIOGLU F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-662926/76.
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                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                              16-JAN-2002
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                                        AAS15806;
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23-MAR-2001; 2001WO-US09410 24-MAR-2000; 2000US-191929P

WO200172962-A2

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The invention relates to substantially pure prostate-specific or testis specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign of the testis or prostate prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The protein of Prostate 1, STMP1, ORF3.
                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Six-Transmembrane Protein of Prostate 1; STWP1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                     760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acctaaggatgccagccggcaggtttatatatgcagcaacaatattcaagcgcgacaaca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggttattgaacttgcccgccagttgaatttcattcccattgacttgggatccttatcatc 180
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                                                                                                                                                                                                                                                                                                                                        Length 2102;
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                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                         Sequence 2102 BP; 595 A; 424 C; 422 G; 661 T; 0 other;
                                                                                                                                                                                                                                                                                                                                        Score 264; DB 22;
Pred. No. 6.7e-128;
                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liver cancer; lung cancer; cytostatic; ss
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/*tag= a
/product= "STMP1"
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                                                                                                                                                                                                                                                                                                                                        65.5%;
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                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.7 Matches 314; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tccatatgctagaaa 315
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                                                                                                                                                                                                                                                                                                                                          Query Match
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The invention relates to substantially pure prostate-specific or testis specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign of the testis or prostate prostatifis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence represents the open reading frame of a prostate protein, Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                               New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 cccagattctttgattgtcaaaggatttaatgttgtctcagcttgggcacttcagttagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     588 cccagattctttgattgtcaaaggatttaatgttgtctcagcttgggcacttcagttagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agccagagagattgaaaatttacccctacgactctttactctctggagagggccagtggt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 65.5%; Score 264; DB 22; Best Local Similarity 99.7%; Pred. No. 6.8e-128; Matches 314; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                             Claim 5; Fig 4D; 114pp; English.
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                                                                                                                               (SAAT/) SAATCIOGLU
                                                                                                                                                                                                               P-PSDB; AAU10187
                                                                                                                                                                Saatcioglu F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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AAS15797 standard; DNA; 528

AAS15797

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Length 1680;

Query Match

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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used include lymphoma, loukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence encodes a prostate specific protein, Six-Transmembrane
                                                                                                                                                                                                                                                                                                                                   Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                    241 ggtagctataagcttggccacattttttttcctttattcctttgtcagagatgtgattca 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pe
                                                                                                                                                                                                                                                                                                  Human cDNA encoding Six-Transmembrane Protein of Prostate 1, STMP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        retractile, ascending or vanished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
178..1650
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product- "STMP1"
                                                                                                                                                                                              AAS15802 standard; cDNA; 1680 BP.
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                                                                                                                                                                                                                                                                     (first entry)
                                                                                         1005 tccatatgctagaaa 1019
                                                                     tccatatgctagaaa 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                   16-JAN-2002
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                                                                                                                                                           RESULT
AAS15802
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Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ss; ORF3.
                                                                                                                                                                                              240
                                                                                                 61 acctaaggatgccagccggcaggtttatatatgcagcaacaatattcaagcgcgacaaca 120
                                                                                                                         707
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                          Gaps
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                                                                          588 cccagattctttgattgtcaaaggatttaatgttgtctcagcttgggcacttcagttagg
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                         Indels
Score 264; DB 22;
Pred. No. 6.7e-128;
0; Mismatches 1;
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/product= "STMP1, ORF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
171..1430
                                                                                                                                                                                                                                                                                                                                                                             AAS15813 standard; cDNA; 2102 BP
  65.5%;
99.7%;
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                          Matches 314; Conservative
                                                                                                                                                                                                                                                                                           301 tecatatgetagaaa 315
                                                                                                                                                                                                                                                                                                        (SAAT/) SAATCIOGLU F.
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               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAU10189
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                Best Local
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Claim 4; Fig 4K; 114pp; English

genetic disorder; ss.

mapping; gene mapping; gene medical imaging; diagnostic;

chromosome

Tang YT;

2000US-0540217 2000US-0649167

forensic;

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                     30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                        Drmanac RT, Liu C,
                                                                                                                                                                                                                               WPI; 2001-639362/73
                                                                                                                                                                                (HYSE-) HYSEQ INC
                       food supplement;
                                                                                                                                                                                                                                           P-PSDB; ABG00113
                                                                      WO200175067-A2
                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                        biodiversity
                                                                                                                                           31-MAR-2000;
                                                                                                                                                        23-AUG-2000;
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                                                                                                                                                              The present sequence is human six transmembrane epithelial antigen of the prostate (STEAP)-2 clone GTD3 cDNA. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is located on chromosome 7g21 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells composition to the patient. Treating a patient with a cancer that comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the single chain monoclonal antibody is expressed intracellularly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                         Ξ
                                                                                             New STEAP (six transmembrane epithelial antigen of the prostate)
proteins, expressed in human cancers, useful for detecting and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1005 ggtagctataagcttggccacatttttttttctttattcctttgtcagagatgtgattca 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agccagagagattgaaaatttacccctacgactctttactcttggagagagggccagtggt 240
                          Faris
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                      present sequence is also shown in sequence listing of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acctaaggatgccagccggcaggtttatatatgcagcaacaatattcaagcgcgacaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                825 acctaaggatgccagccggcaggtttatatatgcagcaacaatattcaagcgcgacaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggtagctataagcttggccacatttttttttcctttattcctttgtcagagatgtgattca
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0
                       Mitchell SC,
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2453;
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2453 BP; 648 A; 537 C; 520 G; 748 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 315; DB 22; L
Pred. No. 1.5e-154;
O; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #104.
                       Saffran DC,
                                                                                                                                                                                                                                                                                                                                                                  specification, but it lacks nulceotides at its
                       Raitano AB,
                                                                                                                                             Claim 4; Fig 9A-9D; 187pp; English
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Conservative 0;
                                                                      P-PSDB; AAE02781, AAE02841
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 (UROG-) UROGENESYS INC
                       Hubert RS,
                                                         WPI; 2001-367804/38
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                    Jakobovits A;
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Best Local Sim
Matches 315;
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                      Afar DEH,
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The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags controlly the expressed genes. (I) is useful in gene therapy techniques controlly or con
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Claim 1; SEQ ID No 104; 103pp; English
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Best Local Similarity 100.
Matches 315; Conservative
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Matches 315;
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Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the protein, antibodies against the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign of the testis or prostate practicularly prostate cancer, benign cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be cancer, pancreatic cancer, breast cancer and lung cancer. The present sequence represents the second open reading frame of a prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents the second open reading frame of a prostate c protein, Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ss; ORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids .
945 ggtagctataagcttggccacattttttttcctttattcctttgtcagagatgtgattca 1004
                                                                                                                                                                                                                                                                                                                                                                                          Human ORF2 of Six-Transmembrane Protein of Prostate 1, STMP1.
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/product= "STMP1, ORF2"
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188..1552
                                                                                                                                                                                                                                     AAS15810 standard; cDNA; 2238 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-662926/76.
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                                                                                                                                                                                                                                                                                                                                      16-JAN-2002
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Length 2238;

Score 315; DB 22; Pred. No. 1.5e-154;

78.2%; S 100.0%;

Query Match Best Local Similarity

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/rag= C
/rag= C
/rag= C
/raduct= "Human six transmembrane epithelial antigen
of the prostate (STEAP)-2, alternative version"
/ransl_except= (pos:1714..1722, aa:Asp-Ala)
/transl_except= (pos:1957..1965, aa:Glu-Gly)
/transl_except= (pos:1957..1965, aa:Glu-Gly)
/transl_except= (pos:2050..2058, aa:Thr-Ser)
/transl_except= (pos:2050..2078, aa:Thr-Ser)
/ransl_except= (pos:2062..2070, aa:Asn-Phe)
/partial
                                                                        ggttattgaacttgcccgccagttgaatttcattcccattgacttgggatccttatdatc 180
                                                                                                                                                                            // ccs "Human six transmembrane epithelial antigen of the prostate (STEAP)-2" 709..2073
                                                                                                                                                    718 ggttattgaacttgcccgccagttgaatttcattcccattgacttgggatccttatcatc 777
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                        cccagattctttgattgtcaaaggatttaatgttgtctcagcttgggcacttcagttagg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytostatic; antiproliferative; vaccine; gene therapy;
six transmembrane epithelial antigen of the prostate-2; STEAP-2;
chromosome 7q21; cancer; prostate; colon; bladder; lung; ovarian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/note= "Kozak region"
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352..358
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WO200175067-A2. Homo sapiens.

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                                                                                                   New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids \,
                                                                                                                                                                                                                                                                                                                                                                                                                  used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence encodes prostate specific protein, Six-Transmembrane Protein of Prostate 1, STMP1, ORF2.
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Pred. No. 1.5e-154;
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                                                                                                                                                                         Claim 4; Fig 4H; 114pp; English.
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Best Local Similarity 100.
Matches 315; Conservative
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                                                 WPI; 2001-662926/76.
                                                                     P-PSDB; AAU10188
                  Saatcioglu F;
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The continuous considerable are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques corresponding a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponshible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human claganostic coding sequences of the invention.

Codingnostic coding sequences of the invention to the printed amino acid sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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23-AUG-2000; 2000US-0649167.
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Matches 315; Conservative
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Location/Qualifiers .188..1552 /*tag= a /product= "STMP1, ORF2"

Homo sapiens

Key

23-MAR-2001; 2001WO-US09410. 24-MAR-2000; 2000US-191929P.

WO200172962-A2

04-OCT-2001.

(SAAT/) SAATCIOGLU F.

Description	Human cDNA encodin	DNA encoding novel	Human ORF2 of Six-	Human six transmem	DNA encoding novel	Human cDNA encodin	Human cDNA encodin	Human ORF of Six-T	Human Six-Transmem
SUMMARIES	AAS15811	AAS76493	AAS15810	AAD07072	AAS64300	AAS15802	AAS15813	AAS15801	AAS15797
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% Query Match Length DB	1561	2192	2238	2453	3900	1680	2102	4329	528
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McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A., Shevchenko,Y., Startipop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                         Direct Submission
Submitted (24-MAR-2000) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Oct 27, 2001 this sequence version replaced gi:7321458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vactor: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Assembly program: Phrap; version 0.990319
Consensus quality: 200596 bases at least 030
Consensus quality: 200596 bases at least 030
Consensus quality: 201000 bases at least 020
Insert size: 197000; agarose-fp
Insert size: 197000; pulse-field-gel
Insert size: 204185; sum-of-contigs
Quality coverage: 9.36x in Q20 bases; pulse-field-gel
Quality coverage: 9.60x in Q20 bases; sum-of-contigs
Quality coverage: 9.03x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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contig of 5025 bp in length
gap of unknown length
gap of unknown length
contig of 13093 bp in length
contig of 13093 bp in length
contig of 11108 bp in length
gap of unknown length
contig of 1377 bp in length
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                                                                                          NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                           Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
------- Project Information
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------ Summary Statistics
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Steed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 6.1e-72;
0; Mismatches 1.
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CORIXA CORPORATION (US)
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                                                                                                                                                                                           /organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_71 c 61 g 106
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AX200582.1 GI:15390402
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ilarity 99.5%;
Conservative
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KEYWORDS
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PAT 22-JUN-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (2028) 1 (2023)
Afar, D.E., Hubert, R.S., Raitano, A.B., Saffran, D.C., Mitchell, S.C.,
Paris, M. and Jakobovits, A.
Serpentine transmembrane antigens expressed in human prostate
cancers and uses thereof patent: WO 0140276-A 11 07-JUN-2001;
Urogenesys, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20508)
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Happinghi, P., Ho, S.-L., IGOl, V.R., Karlins, E., Laric, P., Lee-Lin, S.-G., Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D.,
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            linear
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100.0%; Pred. No. 6.3e-16;
tive 0; Mismatches 0;
               DNA
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322 bp
Sequence 11 from Patent W00140276.
AX155253
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/db_xref="taxon:9606"
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Length 328;

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38.0%; Score 153;

Query Match

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 328)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skelky,Y.A. and Wang,A.
Compositions and methods for the therapy and diagnosis of prostate
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Pred. No. 6.1e-72;
0; Mismatches 1.
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CORIXA CORPORATION (US)
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Ax140722
AX140722.1 GI:14280833
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Sequence 212 from Patent WO0151633.
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/db_xref="taxon:9606"
73 c 61 q 106
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Best Local Similarity
Matches 203; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 328)
Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
Compositions and methods for therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 ttgacttgggatccttatcatcagccagagagattgaaaatttacccctacgactcttta 218
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; '
1 2438: contig of 2438 bp in length 2538: gap of unknown length 1539 8133: contig of 5595 bp in length 1534 8233: gap of unknown length 1234 40378: contig of 32145 bp in length 4078: contig of 13245 bp in length 172915: contig of 132437 bp in length 150cation/Qualifiers
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                                                                                                                              /organism="Papio cynocephalus anubis"
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CORIXA CORPORATION (US)
Location/Qualifiers
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Sequence 212 from Patent W00125272.
AX106431.1 GI:13922110
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31733 c 32277 g 56096
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8234. _40378
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/db_xref="taxon:9606"
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Best Local Similarity 100.
Matches 157; Conservative
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KEYWORDS

SOURCE

REFERENCE AUTHORS

TITLE

JOURNAL

FEATURES

RESULT 10 AX106431

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BASE COUNT ORIGIN

232

173 ttatcatcagccagagagattgaaaatttacccctacgactctttactctggagaggg

233 ccagtggtggtagctataagcttggccacatttttttttcctttattcctttgtcagagat 292

293 gtgattcatccatatgctagaaa 315

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Db 121770 CGACAACAGGTTATTGAACTTGCCGGCCAGTTGAATTTCATTCCATTGACTTGGGATCC 121711
                                                                                                                                                                           Db 121650 CCAGTGGTGGTAGTATAAGCTTGGCCACATTTTTTTTCCTTTATTCCTTTGTCAGAGAT 121591
                                                                                   Db 121710 TTATCATCAGCCAGAGAGATTGAAAATTTACCCCTACGACTCTTTACTCTCTGGAGGG
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Submitted (12-DEC-2001) NIH Intramural Sequencing Center, 8717
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                                                                                                                                                                                                                                                                      Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 161001 bases at least Q40
Consensus quality: 161422 bases at least Q30
Consensus quality: 161562 bases at least Q20
Insert size: 143000; agarose-fp sum-of-contigs Quality coverage: 10.76x in Q20 bases; sum-of-contigs Quality coverage: 9.47x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504 others
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                                                                         Center: NIH Intramural Sequencing Center
Center code: NISC
                           Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                      Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
------ Project Information

    . 162928
    /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-120K11"

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/note-"assembly_fragment"

36349. .66192

/note-"assembly_fragment"

66293. .92168

/note-"assembly_fragment"

/note-"assembly_fragment"
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/note="assembly_fragment
                                                                                                                                                                                                                                                  ----- Summary Statistics
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/note="assembly_fragment
                                                                                                                                                                                                  Center project name: ces
Center clone name: 120K11
                                                       ----- Genome Center
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66293
92169
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                                                  COMMENT
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AC099742 172915 bp DNA linear HTG 20-NOV-2001 Papio cynocephalus anubis clone RP41-167P22, WORKING DRAFT SEQUENCE, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithedinae; Papio.

(bases 1 to 172915)

Akhter, N., Apele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Boietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Ho, S.-L., 10dol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-C.,

McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y.

Stantipop, S., Thomas, J.W., Thomas, P. J., Touchman, J.W.,

Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                    olive baboon.
Papio cynocephalus anubis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 130000; agarose fp
Insert size: 172615; sum-of-contigs
Quality coverage: 12.58x in Q20 bases; agarose-fp
Quality coverage: 9.47x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality; 171178 bases at least 040 Consensus quality; 171910 bases at least 040 Consensus quality; 171910 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@hhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: ccy
Center clone name: 167P22
                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT.
Db 121590 GTGATTCATCCATATGCTAGAAA 121568
                                                                                                                                                                                                                                                                   AC099742.1 GI:17017546
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                                                                                                                                                                                   DEFINITION
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                      ORGANISM
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TITLE
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Gaps

Indels

50.4%; Score 203; DB 2; 1 100.0%; Pred. No. 2.7e-99; .ive 0; Mismatches 0;

Best Local Similarity 100. Matches 203; Conservative

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Query Match

Length 162928;

113 cgacaacaggttattgaacttgcccgctggaatttcattcccattgacttgggatcc 172

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AC104475

162928 bp DNA linear HTG 12-DEC-2001
Pan troglodytes clone RP43-120K11, WORKING DRAFT SEQUENCE, 6
unordered pieces.
AC104475.1 GI:17530717
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                     1 (sites)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Xalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
                                                                                                                                               Compositions and methods for the therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 162928)
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q.,
McCloskey, J.C., Maduro, V.B., Masiello, C., Mastrian, S.D.,
McCloskey, J.C., McDowell, J., Pearson, R., Persad, A., Stantipop, S.,
Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L.,
Malker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and
 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 54.3%; Score 219; DB 6; I
Best Local Similarity 99.6%; Pred. No. 7.6e-108;
Matches 269; Conservative 0; Mismatches 1;
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                                                                                                                                                                           Patent: WO 0173032-A 214 04-OCT-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                          143
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Direct Submission
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Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., wang.A. and Meagher,M.J. Compositions and methods for the therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                  ggttattgaacttgcccgccagttgaatttcattcccattgacttgggatccttatcatc 180
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Pred. No. 7.6e-108;
0; Mismatches 1;
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Sequence 214 from Patent W00151633.
AX200584
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AX267240
AX267240.1 GI:16516018
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/db_xref="taxon:9606"
100 c 78 g 143
                                                                                                                                       241 ggtagctataagcttggccacattttttt 270
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Best Local Similarity 99.6%;
Matches 269; Conservative
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reteed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H., Skeiky,Y.A. and Wang,A. Compositions and methods for the therapy and diagnosis of prostate
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Pred. No. 7.6e-108;
0; Mismatches 1;
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CORIXA CORPORATION (US)
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Sequence 214 from Patent W00134802.
AX140724 1 GI:14280835
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/db_xref="taxon:9606"
100 c 78 g 143

    .444 //Organism="Homo sapiens" //db_xref="taxon:9606"
    .444

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/note="n = A,T,C or
100 c 78 g
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Best Local Similarity 99.6%;
Matches 269; Conservative (
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Best Local Similarity 99.6
Matches 269; Conservative
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Bukaryotas; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 444)
Xu,J.; Skeiky,Y.A.; Reed,S.G. and Cheever,M.A.
Compositions and methods for therapy and diagnosis of prostate cancer
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Best Local Similarity 100.0%; Pred. No. 3e-117;
Matches 236; Conservative 0; Mismatches 0; Indels
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complement(52252. .52467)
                                                                                                                                                                                                                                                     complement(49577. .50216)
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complement(45964...
/rpt_family="L1"
46100...46516
                                                 /rpt_family="L1"
44659 . .44954
/rpt_family="ALU"
45422 . .45448
/rpt_family="L1"
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complement(51721.
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48370. .48785
/rpt_family="L1"
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complement(51765.
/rpt_family="ALU"
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                          /rpt_family="L1"
complement(44380.
                                                                                                                                               complement (45672.
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complement(50540.
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                                                                                                                  complement(45615.
/rpt_family="L1"
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51405. .51691
                                                                                                                                                                                                                                                                                                          complement (50820
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send an E-mail to egreen@nhgri.nih.gov
                                                                       This sequence may not represent the entire insert of this It may be shorter because we only sequence overlapping s once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 978Ks. For references see: Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996).
                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEIGHBORING SEQUENCE INFORMATION: Actual start of this clone is at base position 1 of H_RG016J04; actual end is at 156214 of H_RG016J04. The orientation of this clone is unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone contains STS SWSS2784 (NID:91113580) and SWSS893
http://genome.wustl.edu/gsc
e-mail: sapiens@watson.wustl.edu
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/clone="RG016J04"
/clone_lib="CITB-978SK-B"
15. 40
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/rpt_family="L1"
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/rpt_family="L1"
complement(14777. .14838)
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    156214
    /organism="Homo sapiens"

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/rpt_family="ALU"
complement(9406. .9975)
/rpt_family="L1"
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3398. .342
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/chromosome="7"
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5319. .5345
/rpt_family="L1"
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/rpt_family="ALU"
complement(977. .
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13897. .14096
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complement(25561. .25578)
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27666. .27838
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/note="similar to human EST R09339 (NID:g761262)
yf26d05.r1"
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/note="similar to human EST R09227 (NID:9761150)
                                                                                        mq22f09.rl"
complement(25113. .25148)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .28143)
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40126. .40157
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10007 20922: contig of 916 bp in length 1023 21022: gap of 100 bp 1023 21936: contig of 914 bp in length 937 22036: gap of 100 bp 100 bp 143 23942: contig of 906 bp in length 143 23928: contig of 886 bp in length 29 24028: gap of 100 bp 29 24021: contig of 886 bp in length 20 24021: contig of 886 bp in len
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26883: contig of 896 bp in length
26983: gap of 100 bp
27912: contig of 929 bp in length
28012: gap of 100 bp
28019: contig of 907 bp in length
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25887: contig of 876 bp in length
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54782; contig of 903 bp in length
54882; gap of 100 bp
57769; contig of 887 bp in length
55869; gap of 100 bp
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11 64770: gap of 100 bp
11 5566: contig of 896 bp in length
57 65766: gap of 100 bp
57 66736: contig of 870 bp in length
57 66736: gap of 100 bp
57 66736: gap of 100 bp
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Submitted (09-MAY-1997)
Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, MO 63108, USA
                                                                                                                           58812: gap of 100 bp 59729: contig of 917 bp in length 59829; gap of 100 bp 60738: gap of 100 bp 100
                                                                                                                                                                                                                                                                                              61754: gap of 100 bp
62880: contig of 926 bp in length
62780: gap of 100 bp
63664: contig of 884 bp in length
63764: gap of 100 bp
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in length
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70618: contig of 917 bp in length
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Gattung.S. and Maggi.L.
The sequence of H. saplens BAC clone RG016J04
Unpublished (1997)
2 (bases 1 to 156214)
Waterston.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 236; DB 2; Le
Pred. No. 3.1e-117;
0; Mismatches 0;
                      56836: gap of 100 bp
57715: contig of 879 bp
57815: gap of 100 bp
58712: contig of 897 bp
contig of 867 bp
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100.0%; Pre
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AC021898.2 GI:9119282
HTG. HTG 13-JUL-2000
                                                                 /LTABLAGOTHY GSOPERSISETCLPNGINGINDARKYTVGVIGSGDFAKS
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ASROYYICSNNIQARQQVIELBRQLMFTPIDLGSLSARREIENDELREFTURRGPYVY
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NMAYQVHANIENSWRREEVWRIEMYISFGIMSLGLLSFFFAMVHVAYSLCLPMRRSERYLFL
NMAYQVHANIENSWRREEVWRIEMYISFGIMSLGLLSFFFAMVHOAYSLCLPMRRSERYLFL
ROATGLGSTLGXVALLISFFHYLIYGWRRAFEEEXYRFYTPPNFVLALVYDSIVILDLLQCC
RYPD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone RP11-40708
Unpublished
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/note="unnamed protein product"
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                                     /protein_id="CAC42678.1"
/db_xref="GI:14536714"
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McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thoman, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission

Nubmitted (22-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 13, 2000 this sequence version replaced gi:6730901.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This record contains 88 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: project Information
Center project name: L2445
Center clone name: 407_J_B
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17953: contig of 915 bp in length
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16938: contig of 938 bp in length
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18908: contig of 855 bp in length
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2912: con
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Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Word size :

Searched:

Database :

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AC015723 Homo sapi
AC05549 Homo sapi
AC053948 Homo sapi
AC053951 Homo sapi
AC025691 Homo sapi
AC025691 Homo sapi
AC097064 Homo sapi
AC09791 Homo sapi
AC09791 Homo sapi
AC09799 Homo sapi
AC004477 Lotus jap
U64836 Caenorhabdi
AC100359 Homo sapi
AC100359 Homo sapi
AC100359 Homo sapi
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1 (bases 1 to 2453)

Afar, D.E., Hubert, R.S., Raitano, A.B., Saffran, D.C., Mitchell, S.C., Faris, M. and Jakobovits, A.
Serpentine transmembrane antigens expressed in human prostate cancers and uses thereof
Patent: Wo 0140276-A 7 07-JUN-2001; Urogenesys, Inc. (US)
                                                                                                                          Sequence
Mus muscu
Mus muscu
                                                         Sequence
Pan trogl
Papio cyn
Sequence
                                                                                                                                                                                                                                                                   Homo sapi
Oryza sat
Homo sapi
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Homo sapi
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AC011688 Homo sap1
AF191096 Pneumocys
AC026422 Homo sap1
           Homo sapi
Human BAC
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Homo sapi
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Human DNA
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  Sequence
                   AX106433
AX140724
AX200584
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AC104475
AC099742
AX106431
AX140722
AX26723
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AP001586 H
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AC016853
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Sequence 7 from Patent W00140276.
AXI55249
AXI55249.1 GI:14536713
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/organism="Homo sapiens"
/db_xref="taxon:9606"
355. .1719
AX155249
AC021898
AX106433
AX140724
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AX200584
AX106413
AX106431
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HSJ1060K6
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AC063948
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AC103799
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1935.868 Million cell updates/sec
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                                                                                                                                                                                                           3595312
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                    1797656 seqs, 10463268293 residues
                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                September 20, 2002, 09:52:20
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                                             - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Score

Result . 9 ALS PAGE BLANK (USPTO)

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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 315)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Slam, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCIM0091B19"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0091 row: B column: 19
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                  clone UUGC1M0091B19 R, DNA sequence.
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Location/Qualifiers
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AZ353102.1 GI:10432339
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Fax: 801 585 7177
                                                                                                       house mouse.
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Insert Length: 295 5td Error: 0.00
Seq primer: TACGACTCATAGGGCGAAT
                                                                                                                                                                                                                               EST 01-DEC-2000
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1M0091B19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae; Bos.
1 (bases 1 to 295)
Band,M.R., Larson,J.H., Rebeiz,M., Green,C.A., Heyen,D.W., Donov,J., Windish,R., Steining,C., Mahyuddin,P., Womack,J. and Lewin
                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,H.A. ordered comparative map of the cattle and human genomes Genome Res. 10 (9), 1359-1368 (2000)
                                                                                                                                                                                                                        BF440211 295 bp mRNA linear EST
BS29000195303 Lewin Cattle Spleen Bos taurus cDNA clone
BS29000195303 3', mRNA sequence.
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100.0%; Pred. No. 13;
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/sex="Female"
                  Pred. No. 1.1;
                                      Mismatches
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Location/Qualifiers
1. .295
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100.08; Pt.
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                                                                            276 taaaccagtacccagaatccaa 297
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Fax: 217 244 5617
Email: h-lewin@uiuc.edu
                                                                                                   37 TAAACCAGTACCCAGAATCCAA 16
                                                                                                                                                                                                                                                                                                                  BF440211.1 GI:11500094
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 gblAR129072.1). a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PUDA2NY; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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us-09-802-520-4.rst

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276 taaaccagtacccagaatccaa 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult 8-bay-Embryo library. CDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID-1780077
                                                                                                                                             Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                  1 (bases 1 to 255)

Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                         451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                          On May 7, 1998 this sequence version replaced gi:3121541.
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                                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Sprague-Dawley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13 Forward POLYA=No.
                                                                                           AA957846.1 GI:4277736
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Best Local Similarity
Matches 22; Conserv
                                                                                                                              Norway rat.
                                                                                                                                                                                                                                                                             discovery
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                                                                                                                                                                                                       Rattus.
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AA957846/c
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AUTHORS
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COMMENT
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SOURCE
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                                                                                       VERSION
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Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult 8-Day-Embryo library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amplified cond inserts from a pool of UI-R-EO clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-EO library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B
                                                                                                                                                       EST 09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                    AA957889 343 bp mRNA linear EST 09-MZ
UI-R-E1-fv-a-01-0-UI.S1 UI-R-E1 Rattus norvegicus cDNA clone
UI-R-E1-fv-a-01-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97044477
On May 7, 1998 this sequence version replaced gi:3121584
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Program for Rat Gene Discovery and Mapping
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Location/Qualifiers
37 TAAACCAGTACCCAGAATCCAA 16
                                                                                                                                                                                                                                                              AA957889.1 GI:4277779
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Rattus norvegicus
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ORIGIN
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DB 9; Length 343;

4.5%; Score 22;

Query Match

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Gaps

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22; Conservative

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/organism="Sprague-Dawley"
// Ab_xref="taxon:10116""
// Clone_1ib="U1-R-CO-hr-b-02-0-U1"
// Clone_1ib="U1-R-CO-hr-co-hr-b-02-0-U1"
// Clone_1ib="U1-R-CO-hr-co-hr-b-02-0-U1"
// Clone_1ib="U1-R-CO-hr-co-hr-b-02-0-U1"
// Clone_1ib="U1-R-AI and U1-R-EI clones from which is Stream of the plower of the plower
                                                                                                                                                                                                                                                                                                                                                                                                                            University of lowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 8250
Email: msoares@blue.weeg.ulowa.edu
The sequence tag present in the cDNA between the NotI site and the oligo-df track served to identify it as a clone from the normalized adult 8-Day-Embryo library. CDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics
                                Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                  1 (bases 1 to 242)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                 On Jun 5, 1998 this sequence version replaced gi:3187943.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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97044477
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Location/Qualifiers
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Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
High quality sequence stop: 443.
Location/Qualifiers
I. 516
//db.xefe".taxon.8355".
                                                                                                                                                                                                                                                                                                                                                                                     dablogol.yl NICHD XGC Spl Xenopus laevis cDNA clone IMAGE:4174248 5', mRNA sequence.
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/clone_lib="NICHD XGC Spl"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/lab_host="Shen; Vector: pCMV-SPORT6; Site_l: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.4 kb. Constructed by Life
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
1 (bases 1 to 516)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                        Gaps
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Pred. No. 0.34;
0; Mismatches 0; Indels
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Pred. No. 0.34;
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4.7%; Score 23; DB
Best Local Similarity 100.0%; Pred. No. 0.3
Matches 23; Conservative 0; Mismatches
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Unpublished (1997)
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BG017798
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                                                                                                                                     /clone_lib_NIH_BMAP_M.S.4
//dev_stage="27-32 days" After Technologies)" with a modified /dev_stage="27-32 days" After Technologies)" with a modified /dev_stage="27-32 days" After Technologies)" with a modified /note="Wector: p773D-pac (Pharmacia) with a modified /note="Wector: p773D-pac (Pharmacia) with a modified polylinker; Site_l: Not I; Site_2: Eco RI; The NIH_BMAP_M.S4 library is a subtracted library of a series ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtracted libraries representation of cDNAs from which ESTs had already been generated in this process: NIH_BMAP_M.S4, NIH_BMAP_M.S3.3 NIH_BMAP_M.S3.2, NIH_BMAP_M.S3.2, NIH_BMAP_M.S3.2, and NIH_BMAP_M.S3.3 Lones from which 3: ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M.S3.3, NIH_BMAP_M.S3.2, and NIH_BMAP_M.S3.3. The remaining single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  into DH10B bacteria (LifeTechnologies) to generate the WHLBMAP_W_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1966,
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1 (bases 1 to 502)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
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                                                                                                                        /clone="UI-M-BH3-brx-g-01-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAG_LIB=NIH_BMAP_M_S4
TAG_TISSUE=pineal-glands
                                              /organism="Mus musculus"
                                                                                                /db_xref-"taxon:10090"
  Location/Qualifiers
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                                                                         /strain="C57BL/6J"
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BG019037
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Tumor Gene Index
Tumor Gene Index
Tumor Gene Index
Onpublished (1997)
Other_ESTs: dab27g09.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
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BG557069
BG57069.1 GI:13796858
EST.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 449.
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                                                                                                                                                                                                                                                        /db_xref="taxon:8355"
/clone="IMAGE:4173303"
/clone="InhaGE:4173303"
/clone=lib="wiCHD xGC Spl"
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/dev_stage="adult"
/lab_host="Digne" spleen; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.morhnologies
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1 (bases 1 to 515)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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    502
    /organism="Xenopus laevis"

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108 c
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/clone_lib="Mouse 10kb plasmid UUGC1M library"

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RESULT 7
BI133492/c
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ORIGIN
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                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1M0212F14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0212F14 F, DNA sequence.
AZ428664
GI:10552677
GSS.
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Dunn, D., Aoyaj, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                         4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: F column: 14
Seq primer: GGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 712.
Location/Qualifiers
/tissue_type="head"
/dev_stage="15 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                           168 g
                               /lab_host="DH10B"
                                                                                                                                                                                                                                                                                      170 c
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high moular excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qil4732114)plahet29072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI133492 561 bp mRNA linear EST 02-JUL-2001 UI-M-BH3-brx-g-01-0-UI.sl NIH_BMAP_M_S4 Mus musculus cDNA clone UI-M-BH3-brx-g-01-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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National Institute of Mental Health
National Institute of Mental Health
2080-1943, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
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100.0%; Pred. No. 0.00075;
tive 0; Mismatches 0; Indels
                                                                                                              Laboratory Mouse DNA Resource
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Best Local Similarity 100.0
Matches 28; Conservative
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213 tgtgggacctgagacatctgcttgtggg 240
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//lab.host="DH10B"
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I (bases 1 to 54)

Marrah,, Hiller'L., Kucaba'T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Schurk,R., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,K., S. Shin,T., Jackson,Y., Cardenas,M., McCann,R., Ritter Waterston,R. and Wilson,R. The WashU-NCI Mouse EST Project 1999

Lu Onpublished (1999)

Contact: Marra M/WashU-NI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Park Parkway, Box 8501, St. Louis, MO 63108, USA

Fax: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI747886 541 bp mRNA linear EST 22-JUN-1999 ul03e11.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2065004 5', mRNA sequence.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                             Gaps
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                                                                                                                                                                                                             Length 181;
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                                                         10.5%; Score 52; DB 9; I
Similarity 100.0%; Pred. No. 8.5e-17;
52; Conservative 0; Mismatches 0;
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High quality sequence stop: 498.
Location/Qualifiers
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Gaps

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5.7%; Score 28; DB 9; Length 541; 100.0%; Pred. No. 0.00072; Live 0; Mismatches 0; Indels

Query Match 5.7 Best Local Similarity 100. Matches 28; Conservative

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BB603988 RIKEN full-length enriched, 15 days embryo head Mus
mmusculus CDNA clone D930007L06 5', mRNA sequence.
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishli, Y., Ito, M., Kawai, J., Kohno, H., Kouda (okazaki, Y., Okido, T., Sakai, C., Sakai, K., Shibata, K., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (10 (11), 1757-1771 (2000) (10 (11), 1757-1771 (2000)
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UKL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N. and Hayashizaki,Y.
N., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/db_xref="taxon:10090"
/clone="D930007L06"
/clone_lib="RIKEN full-length enriched, 15 days embryo
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Please visit our web site (http://genome.gsc.riken.go.jp/)
further details.
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On Dec 5, 2000 this sequence version replaced gi:11555390
Contact: Yoshihide Hayashizaki
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                                                    /note="Organ: lung_tumor; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D., Rodfigo F. Chuaqui, M.D., Michael R. Emmert Buck, M.D., Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA888667 131-MAR-1998 nw77b11.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1252605,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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100.0%; Pred. No. v...
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Unpublished (1997)
Conteat: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
/db_xref="taxon:9606"
/clone_lib="ET0211"
                                    /dev_stage="Adult"
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AA888667
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SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-remail.uih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCT-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbpp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA935972 181 bp mRNA linear EST 28-APR-1998
ny30h06.sl NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1273307,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                      /tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
/note="Vector: pAWP10; mRNA made from metastatic prostate lesion of the bone, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prostate
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: pAMP10; mRNA made from metastatic prostatiesion of the bone, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gaverage insert size 600 bp. Library made by D. Krizman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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/lasue_type="metastatic prostate bone lesion"
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8.5e-17;
www-bio.llnl.gov/bbrp/image/image.html
Seg primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.5%; Score 52; DB ilarity 100.0%; Pred. No. 8.5 Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA935972.1 GI:3093129
                                                                                                                                                                                                                  /sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 52; Conserv
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September 20, 2002, 08:33:40 ; Search time 5053.42 Seconds
(without alignments)
1316.732 Million cell updates/sec
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493
1 ggtcactgtaggtgtgattg......ttcccattgacttgggatcc 493
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                               13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                               OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                       Run on:
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gb_gss:* em_gss_hum:* em_gss_inv:* em_gss_pln:* em_gss_vrt:* em_esthum: *
em_estin: *
em_estmu: * em_estov:* em_estpl:* em_estro:* gb_est2:* gb_est1:* gb_htc:* em_htc:* :01

Post-processing: Listing first 45 summaries

em_estba:*

EST:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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S				į														
SUMMARIES	ΩI	BF883142	AA888667	AA935972	AI747886	BB603988	AZ428664	BI133492	BG019037	BG657069	BG017798	AA997082	AA957846	AA957889	BF440211	AZ353102	BF560333	AZ930320
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	& Query Match	79.5	10.5	10.5	5.7	5.7	5.7	5.3	4.7	4.7	4.7	4.5	4.5	4.5	4.1	4.1	4.1	4.1
	Score	392	52	52	28	28	28	56	23	23	23	22	22	22	20	20	20	20
	Result No.	c 1	7	m	4	ស	و ن	c 2	œ	σ	10	c 11	c 12	c 13	14	15	16	17

Tel: +55-11-2704922
Fax: +55-11-270001
Email: sasimpsondibudwig.org.br
This saguence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-ET0211071200-529-bl0&t3=2000-12-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 26
High quality sequence stop: 483.
Location/Qualifiers
1. .483
/organism="Homo sapiens"

source

FEATURES

Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Brazil. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil.

sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663

JOURNAL MEDLINE

COMMENT

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30	5,	w .	250	s .		AV264258 AV264258
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	13	3.9	426	10		BF282857 EST447448
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	19	6.6	499	10	BG894896	BG894896 355672 MA
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					ALIGNMENTS	
RESULT 1						
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LOCUS	BF88	BF883142			483 bp	
DEFINITION	0V3-	ET0211	QV3-ET0211-071200-529-b10	-523	-blo ET0211 Homo sapiens cDNA,	DNA, mRNA sequence.
ACCESSION	PERRIAL4	3142				
VERSION	BFBB	3142.1	5	:122/3268	99	
KEIWOKUS	EST	,				
SOURCE	naman	numan. Homo ganione				
ORGANISM		Sapie	Motoro			1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5
	Mamm	Euraiyota; Mammalia:	Eunalyota, Metazoa, Mammalia: Eutheria:		Cilotata, ciantata, verteblata, Euter Primates: Catarrhini: Hominidae: Homo	idae: Homo.
REFERENCE	1		1 to 483)			
AUTHORS	Dias	Neto,	Dias Neto, E., Garcia	cia	Correa, R., Verjovski-Almeida, S	da, S., Briones, M.R.,
	Naga	i,M.A.	, da Si	lva,	Zago, M.A., Bor	S., Costa, F.F.,
	Gold	man, G.	H., Car	vall	Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala	Bala, G.S., Simpson, D.H.,
	Brun	Brunstein, A.,	A., deo	live	Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,	
	D. M.	., 50a	res, F.,	BIG	ntanı,k.k., keis,L.f., de	souza,s.J. and
(STEP S	Simpson, A. J		,	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 th Open
TITLE	Shot	Shotgun segue seguence tags	quencin	g o	Shotgun sequencing of the human transcriptome with URF sequence tags	ith ORF expressed

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Gaps

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AUTHORS: Sokatch, John R. TITLE: Transcriptional analysis of the promoter region of TITLE: the branched chain keto acid dehyrogenase operon of TITLE: Pseudomonas putida JOURNAL: Journal of Bacteriology
                                                                                                                                                                                                                                             Length 792;
                                                                                                                                                                                                                                             Query Match 3.2%; Score 16; DB 1; Best Local Similarity 100.0%; Pred. No. 28; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: September 20, 2002, 09:51:07 Job time: 11855 sec
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                                                                                                                                                                                                                                                                                                                                                           VOLUME: 172
PAGES: 5655-5663
PATE: 1990
                                                                                                                                                        ; DATE: 15
US-08-403-545-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Genes Encoding Operon and Promoter for TITLE OF INVENTION: Genes Encoding Operon and Promoter for TITLE OF INVENTION: Branched Chain Keto Acid Dehydrogenase of Pseudomonas putida TITLE OF INVENTION: and Methods

TITLE OF INVENTION: and Methods

NUMBER OF INVENTION: 7

CORRESPONDENCES: 7

CORRESSONDENCES: ADDRESS: ADDRESSE: Carolyn D. Moon ADDRESSEE: Dunlap, Codding, Perterson and Lee STREET: 9400 N. Broadway, Suite 420

CITY: Oklahoma City

STATE: Oklahoma
                                                                                                                                                                            .
:0
                                                                                                                                                                                 Gaps
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                                                                                                                              3.2%; Score 16; DB 4; Length 461; 100.0%; Pred. No. 27; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch, 360 Kb Storage COMPUTER: IBM AT OPERATING SYSTEM: MS-DOS Version 3.3 SOFTWARE: Professional Write 2.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Carolyn D. Moon
REISTRATION NUMBER: 33,022
REFERENCE/DOCKET NUMBER: 5820.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: Attorney, (405) 478-5349
TELEFAX: Attorney, (405) 478-5349
                                         /note= "RLG3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7/603/781
APPLICATION NUMBER: 07/172,148
FILLING DATE: 23-003-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                RESULT 15
US-08-403-545-6
Sequence 6, Application US/08403545
Partent No. 5656483
GENERAL INFORMATION:
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LOCATION: 1-792
LOCATION: 1-792
LDENTIFICATION METHOD: Mappin
PUBLICATION INFORMATION:
....HORS: Madhusudhan, K.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 792 Base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double-stranded
TOPOLOGY: Circular
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sokatch, John R. APPLICANT: Sykes, Pamela Joy APPLICANT: Madhusudhan, K.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: Nucleic acid
                                                                                                                            Query Match 3.29
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 Base pairs
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Burns, Gayle
                  CCATION: 1..461
COTHER INFORMATION:
US-09-004-838-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: 0)
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Mayers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CUDNITK: U.S.A.

CIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: F.LOPPY disk

COMPOTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/WS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838

FILING DATE: 09-JAN-1998

CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/10,734

FILING DATE: US-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: EDIADORY, GEOGOTY P.

REGISTRATION NUMBER: 38,440

REGISTRATION NUMBER: 38,440

REGISTRATION NUMBER: 38,440

REGISTRATION NUMBER: 023070-078810US

TELECOMMUNICATION INFORMATION:

METERRENCE/DOCKET NUMBER: 023070-078810US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
              APPLICATION NUMBER: US/08/721,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-004-838-68
Sequence 68, Application US/09004838
Patent No. 6350933
                                                                                                       NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        LENGTH: 374 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.2°
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 461 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 gcttgtgggtaaaatc 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 GCTTGTGGGTAAAATC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two Embarcac
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: CDNA US-08-721-489-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA
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                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Lisa
APPLICANT: Racie, Lisa
APPLICANT: Preacy, Maurice
APPLICANT: Preacy, Maurice
APPLICANT: Spanding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.2%; Score 16; DB 1; Length 374; Best Local Similarity 100.0%; Pred. No. 27; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWRARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,878A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                              ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-824
TELEPHONE: (617) 496-5851
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08721489 Patent No. 5786465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 GCTTGTGGGTAAAATC 97
                                                                                                                                                                                                   Massachusetts: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-686-878A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
                                                                                                                                                                                                                                                02140
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US-08-721-489-1/c
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STATE: Ma
COUNTRY:
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US-08-724-394A-22
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STATE:
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                                                     DB 2; Length 246240; 9.8;
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100.0%; Pred. No. 9.8;
ive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1 TITLE OF INVENTION: Sequences and Antibodies Thereto CORRESPONDENCE: 31 CORRESPONDENCE ADDRESS:
                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA

ZIP: 9411-3834

ZIP: 9411-3834

COMPUTER READBABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A

FILING DATE: 01-0CT-1996

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136

REGISTRATION NUMBER: 35,136

REERENCC/PMOUNTCATION INFORMATION:
TELEPHONE: 415-576-0200

TELEFAM: 415-576-0300

TELEFAM: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ): NAME/KEY: misc_feature

): LCGATION: 1..246240

): OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-21
                                                                                          Mismatches
                                                     Score 17;
Pred. No.
                                                                                                                                                                                                                                                              Sequence 21, Application US/08724394A Patent No. 5872237
                                       3.4%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                     T: Feder, John N.
T: Kronmal, Gregory S.
T: Lauer, Peter M.
T: Ruddy, David A.
T: Thomas, Winston
T: Tromas, Winston
T: Tsuchihashi, Zenta
T: Wolff, Roger K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 atgctgaatatttggct 313
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                                                     Query Match 3.49
Best Local Similarity 100.(
Matches 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
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MOLECULE TYPE:
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US-08-724-394A-20
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US-08-724-394A-21
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                     TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                               ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
. 9.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature

| LOCATION: 1..246240

| OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-22
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ER: 017957-000100
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APPLICATION NUMBER: US/08/724,394A
FILING DATE: U1-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FILES, Renee A.
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 017957-0001C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NO. 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 24640 base pairs
Sequence 22, Application US/08724394A Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 47, Application US/08686878A Patent No. 5708157
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.4%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                  APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winsten
BPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
                                        GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS: not relevant not relevant
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LaVallie, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Racie, Lisa
Merberg, David
Treacy, Maurice
Evans, Cheryl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: not r
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-08-686-878A-47/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
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FEATURE

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 7705;
8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                       HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 3' END OF RAD50 GENOMIC SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: 35,136
ATORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.4%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 8.6 Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-724-394A-20; Sequence 20, Application US/08724394A; Patent No. 5872237; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Feder, John N. APPLICANT: Kronmal, Gregory S.
                               115:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: not relevant
GY: not relevant
                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: 20:
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 7705 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7390 ATGTCACTCATCATGAA 7406
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                                                                                                                                                                                                                                                                                                                                        US-08-687-080-115
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Patent No. 5965427
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 3.7%; Score 18; DB 3; Length 4447; Best Local Similarity 100.0%; Pred. No. 2.4; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/687,080 FILING DATE: 17-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : NAME/KEY: misc_feature

: LOCATION: 1..447

: OTHER INFORMATION: /product= "Pig DPD"

US-08-991-942-3
                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/304,309
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
RESISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 15280-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                             APPLICATION NUMBER: US/08/991,942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 460
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3258 AAAACAAATATAATATT 3275
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  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 88..3162
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 350 TTY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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APPLICANT: GONZALEZ, Frank J.
APPLICANT: FERNANDEZ-SALGUERO, PEDRO
TITLE OF INVENTION: CLONING AND EXPRESSION OF CDNA FOR HUMAN
TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
    DIHYDROPYRIMIDINE DEHYDROGENASE
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATIS: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/304,309
FILING DATE: 09-SEP-1994
CLASSIFICATION: 435
                                              STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.7%; Score 18; DB 2;
100.0%; Pred. No. 2.4;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: 1.4447
; OTHER INFORMATION: /product- "Pig DPD"
US-08-304-309-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08991942 Patent No. 6015673 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35.367
REFERENCE/DOCKET NUMBER: 15.
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3258 AAAACAAATATAATATT 3275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 aaaacaaatataattt 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                            94105-1493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-991-942-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 aggatgccagccggcaggtttatatatgcagcaacaatattcaagcgcgacaacaggtta 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 attetttgattgteaaaggatttaatgttgteteagettgggeaetteagttaggaeeta 386
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GONZALEZ, Frank J.
APPLICANT: FERNANDEZ-SALGUERO, PEGTO
TITLE OF INVENTION: CLONING AND EXPRESSION OF CDNA FOR HUMAN
                                                                                                                                                                                                                                                                                                     28.2%; Score 139; DB 4; Length 328; 100.0%; Pred. No. 3e-66; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.9%; Score 19; DB 3; Length 1648; 100.0%; Pred. No. 0.66; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-165-241-2/c

| Sequence 2, Application US/09165241
| Patent No. 6130077
| GENERAL INFORMATION:
| APPLICANT: Henry Vue
| APPLICANT: Karl J. Guegler
| APPLICANT: Neil C. Corley
| APPLICANT: Neil C. Corley
| APPLICANT: Janice Au-Young
| TILE OF INVENTION: HUMAN CYTOCHROME P450
| FILE REFERENCE: PF-0608 US
| CURRENT RPLICATION NUMBER: US/09/165,241
| CURRENT FILING DATE: 1998-10-01
| NUMBER OF SEQ ID NOS: 2
| SOFTWARE: PERL PROGRAM
| SFO IT NO. 1
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SSOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 328
                                                                                                                                                                         : NAME/KEY: misc_feature

: LOCATION: (1)...(328)

: OTHER INFORMATION: n = A,T,C or G

US-09-439-313-212
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Patent No. 5856454
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 139; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE: -
; OTHER INFORMATION: 991729
US-09-165-241-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                  LENGTH: 328
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2
LENGTH: 1648
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US-08-304-309-3
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447
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Gaps

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ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fanger, Gary
Retter, Mark
Solk, John
                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                              CORRESPONDENCE ADDRESS:
                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-030-607-212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                           STREET: 6300 Co
CITY: Seattle
STATE: WA
                                                                                                                                          USA
                                                                                                                                                       98104
                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-439-313-212
                                                                                                                                          COUNTRY:
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APPLICANT:
APPLICANT:
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345 gatttaatgttgtctcagcttgggcacttcagttaggacctaaggatgccagccggcagg 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tttatatatgcagcaacaatattcaagcgcgacaacaggttattgaacttgcccgccagt 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.4%; Score 209; DB 4; Length 444; 100.0%; Pred. No. 2.4e-104; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            THERAPY AND
                                                                                                                                                                                                                                                          GENERAL INCOMMATION:
APPLICANT: XU, Jiangchun
APPLICANT: XU, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Ralos, Michael
APPLICANT: Ralos, Michael
APPLICANT: Reter, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF SEQ ID NOS: 575
CURRENT FILING DATE: 1999-11-12
SOUTHWARE: FastSEQ for Windows Version 3.0
                                                                                                                          465 tgaatttcattcccattgacttgggatcc 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 212, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
                                                                                                                                                                                                                                 Sequence 214, Application US/09439313
Patent No. 6329505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)...(444)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100. Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-030-607-212
                                                                                                                                                                                                                      US-09-439-313-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 214
LENGTH: 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fcore 135,
Pred. No. 3e-66;
0;
                                                                                                 SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.2%; Score 139; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 212:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 212, Application US/09439313
Patent No. 6229505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
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GenCore version 4.5

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 09:49:23; Search time 139.75 Seconds

(without alignments)

866.528 Million cell updates/sec

Title: US-09-802-520-4

Perfect score: 493
Sequence: 1 ggtcactgtaggtgtattg......ttcccattgacttgggatcc 493
Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066
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Database : Issued_Patents_NA:*

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 214, App		212,	212,	2, A	'n	3,	11	20,	21,	22,	47,	1, 7	68	, ,9	Sequence 6, Appli	1,	Ļ	3,	Sequence 3, Appli	ì	3	Sequence 25, Appl	9	25,	7	7
SUMMARIES	ID	US-09-030-607-214	US-09-439-313-214	US-09-030-607-212	US-09-439-313-212	US-09-165-241-2	US-08-304-309-3	US-08-991-942-3	US-08-687-080-115	US-08-724-394A-20	US-08-724-394A-21	US-08-724-394A-22	US-08-686-878A-47	US-08-721-489-1	US-09-004-838-68	US-08-403-545-6	US-08-404-381-6	US-08-869-506-1	US-09-128-967-1	US-09-450-852-3	US-08-511-485-3	US-09-392-580-1	US-09-175-928-3	US-08-117-491-25	US-08-271-364A-6	US-08-222-715B-25	US-08-343-760A-1	US-08-004-139B-2
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             Length 539;
                            Indels
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                            Mismatches
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2000US-0207456.
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2000US-0234559.
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                            Conservative
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                     Similarity
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                             The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                               ggtcactgtaggtgtgattggaagtggagattttgccaaatccttgaccattcgacttat 182
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Pred. No. 1.4e-203;
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                                                                                                                                                                       Claim 25; SEQ ID No 17799; 654pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leuksemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 taaaatcctgattgatgtgagcaataacatgaggataaaccagtacccagaatccaatgc 422
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                                                                                                                                                                                                                           gene expression analysis; probe;
                    Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO: 17595; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                    Human bone marrow expressed single exon probe SEQ ID NO: 17595
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                                                             cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analyzing gene expression in human bone marrow
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                                                                                                                                                                                                                         Human; bone marrow microarray; cancer;
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(SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human single exon nucleic acid probes
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                                                                                                                                                                                                                                                                                                                                                                                     human; microarray; gene expression; cervical epithelial cell;
                                                                                       Human genome-derived single exon nucleic acid probes useful fanalyzing gene expression in human cervical epithelial cells
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27-SEP-2000;
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                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for
                                                                                                                                                                                                                                                                                                predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human
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ive 0; Mismatches 0;
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                                                                                                                                                            Rank DR;
                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
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                                                   20000S-0207456.
20000S-0608408.
20000S-0632366.
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21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tagatgoggctatcatgtggtcataggaagtagaaatcctaagtttgcttctgaatttt 120
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                                                                                                                                                                 Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgttgctatacacagagaacattatacctccctgtgggacctgagacatctgcttgtggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 539;
                                                                                                                         Human brain expressed single exon probe SEQ ID NO: 17240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 405; DB 22; I Pred. No. 1.4e-203;
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100.0%; Pre
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2000US-0207456.
2000US-0608408.
2000US-063286.
2000US-0234687.
  539
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                                                                                  (first entry)
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    DNA;
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AAK17249 standard;
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30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000;
27-SEP-2000;
                                                                                05-NOV-2001
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Best Local Si
Matches 405;
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                                                                                                                                                                                                                                                                                                                                                                                                                               probe; ss
than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                             362
                                                                                                                        240
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                                                                                                                                                                                                                                                                                  taaaatcctgattgatgtgagcaataacatgaggataaaccagtacccagaatccaatgc 300
                                                                                                                                                                                                                                                                          tgaatatttggcttcattattcccagattcttgattgtcaaaggatttaatgttgtctc 360
                                                                                                 Gaps
                                                                                                                1 ggtcactgtaggtgtggattggaagtggagattttgccaaatccttgaccattcgacttat 60
                                                                                                                                                                                                           Human; foetal liver; gene expression; single exon nucleic acid
                                                                                                0;
                                                                                Length 539;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                              foetal liver single exon nucleic acid probe #17222
                                                                                                                                                                                                                                                                                                       Sequence 539 BP; 156 A; 96 C; 118 G; 169 T; 0 other;
                                                                               tch 82.2%; Score 405; DB 22; I al Similarity 100.0%; Pred. No. 1.4e-203; 405; Conservative 0; Mismatches 0;
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2000US-0608408.
2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                               ABA68917 standard;
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03-AUG-2000;
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04-OCT-2000;
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                                                                                Query Match
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                                                                                         Local
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 539;
                                                                              single exon nucleic acid probes useful
                                                                                                                                     Claim 4; SEQ ID NO 17222; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, gene expression, heart, microarray, vascular system, cardiovascular disease, hypertension, cardiac arrhythmia, congenital heart disease, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 539 BP; 156 A; 96 C; 118 G; 169 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 82.2%; Score 405; DB 22; I
llarity 100.0%; Pred. No. 1.4e-203;
Conservative 0; Mismatches 0;
                                                                                                  analyzing gene expression in human fetal
DR;
  Rank
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Chen W,
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Hanzel DK,
                                                                              Human genome-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 405; Conserv
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Penn SG,
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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them.
Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the protein, antibodies against the proteins. Compounds that modulate the prostate specific or testis of the nucleic and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign of the testis or prostate prostatifis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, the cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence represents the open reading frame of a prostate presentic specific protein, Six-Transmembrane Protein of Prostate 1, STMP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tagatgoggotatoatgtggtcataggaagtagaatcotaagtttgottotgaattttt 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 493; DB 22;
100.0%; Pred. No. 5.4e-250;
ive 0; Mismatches 0;
                                                                                                        Location/Qualifiers
178..1650
                                                                                                                                              /*tag= a
/product= "STMP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Fig 4D; 114pp; English.
                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09410.
                                                                                                                                                                                                                                                                                                     24-MAR-2000; 2000US-191929P.
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                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                        (SAAT/) SAATCIOGLU F.
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P-PSDB; AAU10187.
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                                                                                                                                                                                              WO200172962-A2
                                                                                                                                                                                                                                                                                                                                                                         Saatcloglu F;
                                                                         Homo sapiens
                                                                                                                                                                                                                                 04-OCT-2001
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contecting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias
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sample derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from humar
                                                                                                                                                                                                                                                                                                                                                                                                                            microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          breast, comprises number of single exon nucleic acid probes
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                                                                                                                                                                                                                                                                                                                                                                                              Human breast cell single exon nucleic acid probe #9633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
                                                                                                                                                                                                                                                                                                              ABA50938 standard; DNA; 539 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         disease; cancer; ss
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
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us-09-802-520-4.rng

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                     240
                                                                                                                                                        420
                   623
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                                                                                                                                                                                             taaaatcctgattgatgtgagcaataacatgaggataaaccagtacccagaatccaatgc
                                                                                    tgaatatttggcttcattattcccagattctttgattgtcaaaggatttaatgttgtctc
                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                               novel human diagnostic protein #104
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                                                                                                                                                                                                                                                                                                        BP.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
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for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and among acid sequences. AAS64197-AAS94564 represent novel human call sequences of the invention.

Specification, but was obtained in electronic format directly from MIPO
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                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                        Sequence 3900'BP; 1161 A; 798 C; 892 G; 1049 T; 0 other;
                                                                                                                                                                                                                                                                                                    Score 493; DB 23;
Pred. No. 5.4e-250;
                                                                                                                                                                                                                                                                                    100.0%; Score
100.0%; Pred. No. 5...
0; Mismatches
                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                            Gaps
                                                                                                                                           specific polypeptide are useful to diagnose, prevent or treat disor of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence represents the second open reading frame of a pros specific protein, Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human six transmembrane epithelial antigen of prostate-2 clone GTD3
                                                                                                                                                                                                                                                                                     tgttgctatacacagagaacattatacctccctgtgggacctgagacatctgcttgtggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytostatic; antiproliferative; vaccine; gene therapy;
six transmembrane epithelial antigen of the prostate-2; STEAP-2;
chromosome 7q21; cancer; prostate; colon; bladder; lung; ovarian;
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                                                                                                            Length 2238;
                                                                                                                            Indels
                                                                                   Sequence 2238 BP; 607 A; 457 C; 453 G; 721 T; 0 other;
                                                                                                          100.0%; Score 493; DB 22;
100.0%; Pred. No. 5.3e-250;
ive 0; Mismatches 0;
                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
352..358
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                                                                                                                           493; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     481 tgacttgggatcc 493
                                                                                                                   Similarity
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                                                                                                           Query Match
Best Local 3
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The present sequence is human six transmembrane epithelial antigen of the prostate (STEAP)-2 clone GTD3 cDNA. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is located on chromscome 7q21 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and panoreatio) expressing STEAP or inhibiting growth or killing cells expresses STEAP in a patient. Treating a patient with a cancer that composition to the patient. Treating a patient with a cancer that composition to the patient. Treating a patient with a cancer that composition to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and such that the vector delivers the single chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal antibody is expressed intracellularly.
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proteins, expressed in human cancers, useful for detecting and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitchell SC, Faris M;
                                                              of the prostate (STEAP)-2"
                                                                                                                                                                                                                                                transmembrane epithelial antigen
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                                                                                                                                                                                                                                      /product= "Human six transmembrane epithelial antigen of the prostate (STEAP)-2, alternative version"
/note= "CDS does not include start and stop codon"
/transl_except= (pos:1714..1722, aa:Asp-Ala)
/transl_except= (pos:1834..1842, aa:Asp-Ala)
/transl_except= (pos:1957..1965, aa:Arg-Ser)
/transl_except= (pos:2050..2058, aa:Thr-Ser)
/transl_except= (pos:2050..2058, aa:Thr-Ser)
/note= "Inframe stop codon alters the reading frame"
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100.0%; Pred. No. 5.4e-250;
iive 0; Mismatches 0;
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"Kozak region"
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome, and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical assorbides involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in changing the constant of mattations constant in the constant of mattations in the protein and constant of adaquostics, forensics, gene mapping, identification of mattations of a protein constant of a polypeptide constant of a polyperior o
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from W1
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                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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23-AUG-2000; 2000US-0649167
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                                                                                                           Homo sapiens.
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Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer, benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ss; ORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
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               taaaatcctgattgatgtgagcaataacatgaggataaaccagtacccagaatccaatgc
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171..1430
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Also included are vectors and host cells expressing the proteins are transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, panoreatic cancer, liver cancer and lung cancer. The present sequence encodes prostate specific protein, six-transmembrane protein of Prostate 1, STMP1, ORF3.
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100.0%; Pred. No. 5.3e-250;
ive 0; Mismatches 0;
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  4K; 114pp; English.
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493; Conserv
Fig
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standard; cDNA; 1680 BP

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(first entry)

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Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benjan prostatic hypersplasia; acute prostatitis; testicular aancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
                                                                                                                         Human cDNA encoding Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                             liver cancer; lung cancer; cytostatic; ss.
                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                     16-JAN-2002
                  AAS15802
                                                    AAS15802;
AAS15802
                                     testis specific polypeptides and the nucleic acids encoding them.

Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign of the testis or prostate prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence encodes prostate specific protein, Six Transmembrane or protein of Prostate 1, STMP1, ORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                 New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        taaaatcctgattgatgtgagcaataacatgaggataaaccagtacccagaatccaatgc 300
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                                                                                                                       prostate-specific or testis-specific nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 493; DB 22; 100.0%; Pred. No. 5.3e-250;
                                                                                                                                                                                          invention relates to substantially pure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                        Claim 4; Fig 4H; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 493; Conservative
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                               WPI; 2001-662926/76.
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                                                  P-PSDB; AAU10188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence encodes a prostate specific protein, Six-Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 493; DB 22;
Pred. No. 5.3e-250;
Mismatches 0;
Location/Qualifiers
178..1650
                                                                                         /product= "STMP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 4E; 114pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                                                                                                       24-MAR-2000; 2000US-191929P.
                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09410.
                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                   (SAAT/) SAATCIOGLU F.
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P-PSDB; AAU10187.
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Best Local Similarity
                                                                                                                                                            WO200172962-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saatcioglu F;
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1 ggtcactgtaggtgtgattg.....ttcccattgacttgggatcc 493
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                   1736436 segs, 858457221 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

vo.	Description	Human cDNA encodin	Human cDNA encodin	Human cDNA encodin	DNA encoding novel	Human ORF2 of Six-	Human six transmem	DNA encoding novel	Human ORF of Six-T	Human breast cell
SUMMARIES	ΩI		AAS15802	AAS15813	AAS76493	AAS15810	AAD07072	AAS64300	AAS15801	ABA50938
	DB	22	22	22	23	22	22	23	22	22
	e Match Length DB	1561	1680	2102	2192	2238	2453	3900	4329	539
ap (Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	82.2
	Score	493	493	493	493	493	493	493	493	405
	NO.	П	7	٣	4	S	9	7	8	6

23-MAR-2001; 2001WO-US09410. 24-MAR-2000; 2000US-191929P.

04-OCT-2001.

(SAAT/) SAATCIOGLU F.

10	405	ζ.	539	22	ABA68917		Human foetal liver
11	405	· '	539	22	ABA35870		#14336
12	405	~ ·	υ υ υ	7.7	AAK1/249		brain
ET.	405	· (ט ני ט ני	77	AAK43038		Done marrow
1 T	4 C V	'nς	200	77 0	AA123801		Probe #13/34 LOF 9 Probe #17799 used
11.	4 0 0	• •	000	2 0	AATO9410		#9401
17	4 0 5		72	22	AAS15793		DNA fo
18	405	i	95	22	ABA45820		breast
19	405	2	95	22	ABA56335		Human foetal liver
20	405	ď.	95	22	ABA25976		Probe #4442 for ge
21	405	ά.	95	22	AAK04514		Human brain expres
22	405	ď.	95	22	AAK30016		Human bone marrow
23	405	82.2	1953	22	AAI14606	r	Probe #4539 for ge
24	405	ö	95	22	AAI35978		Probe #4664 used t
25	405	ς.	95	22	AAI04420		Probe #4411 used t
26	403	÷	525	22	AAS15796		Human Six-Transmem
27	403	÷	525	22	AAS15805		Human Six-Transmem
28	209	ď.	444	19	AAV61348		Forward DNA sequen
58	209	2	444	13	AAV58684	ř	Prostate tumour sp
30	508	'n	444	21	AAA06447		Human immunogenic
31	209	'n	444	22	AAS63655		Human prostate cDN
32	209	ς.	444	22	AAS10206		Human prostate tum
33	209	ď	444	22	AAH93563		Human prostate-spe
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4.2	139	· œ	328	7.7	AAH84875		rostate-s
43	139	ω,	328	22	AAH02626	•	െ–
44	06	18.3	528	22	AAS15797	• .	Human Six-Transmem
45	06	8	528	22	AAS15806	. ,	Human Six-Transmem
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RESULT	1						
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ID AAS1	5811	standard;	; cDNA;	1561	. BP.		
AC AAS	AAS15811;						
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1	7007 NUO						
	Human cDNA	encoding	ng ORF2	of	Six-Transmembrane	embrane Protein	n of Prostate 1.
××							
	Human; Six-	Transme	embrane	Prot		Prostate 1; STMP1	TMP1; prostate cancer;
	benign pros	tatic	prostatic hyperplasia; acute	asia,	Д		
	cryptorchidism; test	lism; to	esticul	ar di	testicular disorder; p	erative d	sorder; lymphoma;
	ıkaemia;	melano	na; ova	rian		reast cancer;	pancreatic cancer;
4	iver cancer	funt (1	rancer f		cytostatic;	n n	
OS Homo	o sapiens	. 81					
FH Key		ŭ÷	ocation 155	/Qua	itiers		
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/note="assembly_fragment clone-end:r7 vector_side:left"

wisc_feature 109756. .227144
/note="assembly_fragment"

BASE COUNT 68114 a 46378 c 46791 g 65638 t 223 others
ORIGIN
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Search completed: September 20, 2002, 09:52:20 Job time: 12998 sec

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Mus musculus
                                                                                                                                                                                     house mouse.
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                                   NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Quality coverage: 9.60x in Q20 bases; pulse-field-gel
Quality coverage: 9.03x in Q20 bases; sum-of-contigs
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100.0%; Pred. No. 0.0001;
ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                             s: contig of 4428 bp in length

s: gap of unknown length

s: contig of 5025 bp in length

s: contig of 13093 bp in length

s: contig of 13093 bp in length

s: gap of unknown length

s: contig of 11108 bp in length

s: gap of unknown length

s: contig of 13777 bp in length

s: gap of unknown length

s: gap of unknown length

s: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                       109919: contig of 28030 bp in length 110019: gap of unknown length 153235: contig of 42136 bp in length 153335: gap of unknown length 205085: contig of 51750 bp in length.
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1. 4428
1. 4428
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1. 4529. 9533
7. 00te="assembly_fragment"
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gap of unknown length
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gap of unknown length
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a 40716 c 41296 g 61026 t
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/note="assembly_fragment"
81890. .10919
/note="assembly_fragment"
110020. .153235
/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment

    .205085
    /organism="Mus musculus"
    /strain="C57BL6/J"

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/chromosome="5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Best Local Similarity 100.0
Matches 28; Conservative
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9554
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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AC092404 227144 bp DNA linear HTG 04-JUL-2001 Mus musculus chromosome 5 clone RP23-261D18 strain C57BL6/J, WORKING DRAFT SEQUENCE, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 227144)
Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Ho,S.-L., Idol,J.R., Karlins,E., Lee-Lin,S.-Q., Legaspi,R., Lin,M., Maduro,Q.L., Maduro,V.B., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A., Shevchenko,Y., Snyder,B., Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (04-JUL-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: 261D18

Center clone name: 261D18

Center clone name: 261D18

Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.990319
Assembly program: Phrap; version 0.990319
Consensus quality: 225959 bases at least Q30
Consensus quality: 225959 bases at least Q30
Consensus quality: 2259678 bases at least Q30
Consensus quality: 2259679 bases at least Q30
Insert size: 225000; agarose-fp
Insert size: 225000; pulse-field-gel
Insert size: 126944; sum-of-contigs
Quality coverage: 12.84x in Q20 bases; sun-of-contigs
Quality coverage: 12.73x in Q20 bases; sum-of-contigs
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26808: gap of unknown length
109655: contig of 82847 bp in length
109755: gap of unknown length
227144: contig of 117389 bp in length.
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/clone_lib="RPCI mouse BAC library 23"
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Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---- Project Information
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                                                                                                                                               AC092404.1 GI:14595778
HTG; HTGS_PHASE1; HTGS_DRAFT.
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us-09-802-520-4.rge

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96 35995; gap of 100 bp 13640; see 136840; contig of 845 bp in length 13640; gap of 100 bp 100 bp 137822; contig of 882 bp in length 137822; gap of 100 bp 100 bp 16 38945; gap of 100 bp 16 39923; contig of 878 bp in length 16 39923; contig of 869 bp in length 16 40792; contig of 869 bp in length 16 39923; gap of 100 bp 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 3923: gap of 100 bp 
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                                                                                                                                       100 bp
878 bp in length
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47713: contig of 852 bp in length
48729: contig of 916 bp
48729: contig of 916 bp in length
48729: contig of 916 bp in length
49779: contig of 950 bp in length
                                                                                                                                                                                                         100 bp
E 888 bp in length
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                         30033: gap of 100 bp 30930: contig of 897 bp in length 31030: gap of 100 bp 31924: contig of 894 bp in length
                                                                                                                                                                                                                                                                     ap of 100 bp in length contig of 910 bp in length
                                                                                                                                                                                                                                                                                                                                 35000: gap of 100 bp
35895: contig of 895 bp in length
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56736: contig of 867 bp in length
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3 41811: contig of 91
2 41911: gap of 100
12 42806: contig of 86
                                                                                                                                                                                                      3 33002: gap of 100
3 33890: contig of 8
1 33990: gap of 10
11 34900: contig of 9
οţ
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32902: contig of
      contig
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60638: con+
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62680: cont
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205085 bp DNA linear HTG 27-OCT-2001 Mus musculus chromosome 5 clone RP23-119M19 strain C57BL6/J, WORKING DRAFT SEQUENCE, 10 unordered pieces.
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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.; Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haqhighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-O., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y. Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Taurgeon, C., Vogt, J.L., Malker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L., H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24-MAR-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Oct 27, 2001 this sequence version replaced gi:7321458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 199516 bases at least 040
Consensus quality: 200596 bases at least 030
Consensus quality: 201000 bases at least 020
Insert size: 197000; agarose-fp
Insert size: 192000; pulse-field-gel
Insert size: 204185; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 87401;
57 65766: gap of 100 bp 6536: contig of 870 bp in length 100 bp 1
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Contact: nisc_mouse@nhgri.nih.gov
------ Project Information
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100.0%; Pred. No. ...
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                                              ggctatcatgtggtcataggaagtagaaatcctaagtttgcttctgaatttttcctcat 127
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Center: Whitehead Institute/ MIT Center for Genome
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  4; Indels
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Web site: http://www-seq.wi.mit.edu
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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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9906: contig of 893 bp in length

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10906: contig of 900 bp in length

06: gap of 100 bp

11910: contig of 904 bp in length
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Dietrich, N. L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hos, S.-L., Idol, J. R., Karlins, E., Laric, P., Lee-Lin, S.-G., Legaspi, R., Maduro, Q. L., Maduro, V. B., Masiello, C., Mastrian, S. D., McCloskey, J. C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Stantripop, S., Thomas, J. W., Thomas, P. J., Touchman, J. W., Tsurgeon, C., Vogt, J. L., Walker, M. A., Wetherby, K. D., Wiggins, L., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                         Submitted (20-NOV-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                Center: NIH Intramural Sequencing Center
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98.8%;
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                                                                                                                                                                                      Green, E.D.
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC099742 172915 bp DNA linear HTG 20-NOV-2001 Papio cynocephalus anubis clone RP41-167P22, WORKING DRAFT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Papio cynocephalus anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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1 (bases 1 to 172915)
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
                                                                          104 AGGATGCCAGCCGGCAGGTTTATATATATGCAGCAACAATATTCAAGCGCGACAACAGGTTA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aggatgccagccggcaggtttatatatgcagcaacaatattcaagcgcgacaacaggtta 446
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                                                                                                                                                                                                                                                             DNA
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CORIXA CORPORATION (US)
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                                                                                                                                                                                                                                                      Sequence 212 from Patent W00173032. AX267238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
73 c 61 g 106
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                           447 ttgaacttgcccgccagtt 465
                                                                                                                                                  164 TIGAACTIGCCCGCCAGTI 182
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AX267238
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AC099742
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 17170% bases at least Q40 consensus quality: 171910 bases at least Q30 consensus quality: 172336 bases at least Q20 lnsert size: 130000; agarose-fp insert size: 172615; sum-of-contigs Quality coverage: 12.58x in Q20 bases; agarose-fp Quality coverage: 9.47x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
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4 8133: contig of 5595 bp in length
4 40378: contig of 32145 bp in length
4 40378: contig of 32145 bp in length
9 172915: contig of 132437 bp in length.
Location/Qualifiers
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/organism="Papio cynocephalus anubis"
/db_xref="taxon:9555"
/clone="RP41-167P22"
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Pred. No. 6.9e-68;
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/note="assembly_fragment"
1 31733 c 32277 g 56096 t
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/note="assembly_fragment
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PAT 29-AUG-2001
                                                                       Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 328)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Sked,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skelky,Y.A. and Wang,A.
Compositions and methods for the therapy and diagnosis of prostate
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1 (bases I to 328)

Xu,J. Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Steed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
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CORIXA CORPORATION (US)
Location/Qualifiers
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100.0%; Pred. No. 4e-
iive 0; Mismatches
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 Sequence 212 from Patent WO0134802
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                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
73 c 61 a 106
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/db_xref="taxon:9606"
73 c 61 q 10
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Location/Qualifiers
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AX140722.1 GI:14280833
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Matches 139; Conservative
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                                                                     Query Match 42.4%; Score 209; DB 6; Le Best Local Similarity 100.0%; Pred. No. 8.1e-113; Matches 209; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 4e-71;
ive 0; Mismatches 0.
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1 (bases 1 to 444)

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H., Skeiky,Y.A. and Wang,A.

Compositions and methods for the therapy and diagnosis of prostate
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 444)

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,W.D., Panger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of prostate
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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CORIXA CORPORATION (US)
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CORIXA CORPORATION (US)
Location/Qualifiers
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Sequence 214 from Patent W00151633. AX200584 AX200584.1 GI:15390404
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Pan troglodytes clone RP43-120K11, WORKING DRAFT SEQUENCE, 6
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1 (bases 1 to 16298)
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haphighi, P.,
Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q.,
Hcgaspi, R., Maduro, O.L., Maduro, V.B., Masiello, C., Mastrian, S.D.,
McCloskey, J.C., McDowell, J., Pearson, R., Parsad, A., Stantripop, S.,
Thomas, J.W., Thomas, P. J., Touchman, J.W., Tsurgeon, C., Vogt, J.L.,
Malker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-DEC-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap, version 0.990319
Consensus quality: 161402 bases at least Q40
Consensus quality: 161422 bases at least Q30
Consensus quality: 161562 bases at least Q20
Insert size: 143000; agarose-fp
Insert size: 16428; sum-of-contigs
Ouality coverage: 10.76x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center code: NISC
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HTG; HTGS_PHASE1; HTGS_DRAFT
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92268:
122036:
122136:
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                                                                                    unordered pieces
                                                                                                                                                                                             Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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36249
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92169
122037
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                                                                                                                                                                        chimpanzee
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RESULT 3
AC104475/c
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KEYWORDS
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                                                                                                                                                                                                                                                                               AUTHORS
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/organism="Pan troglodytes"

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PAT 30-APR-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37789 GGTCACTGTAGGTGTGTGTAGAGTGGAGATTTTGCCAAATCCTTGACCATTCGACTTAT 37730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 tagatgcggctatcatgtggtcataggaagtagaaatcctaagtttgcttctgaattttt 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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99.7%; Pred. No. 3.6e-169;
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Patent: WO 0125272-A 214 12-APR-2001;
CORIXA CORPORATION (US)
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                                                                                                                                                                       /note="assembly_fragment"
66293 .92168
/note="assembly_fragment"
92269 .122036
/note="assembly_fragment"
122137 .162928
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                    /note="assembly_fragment" 36349. .66192

    13922
/note="assembly_fragment

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29878 c 30533 g
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                                                                                                                       .36248
                                                                                     clone_end:T7
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                                                                                                                         14023.
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repeat_region 4012640157 repeat_region /rpt_family="L1" repeat_region /rpt_family="ALU" repeat_region /rpt_family="L1" repeat_region /rpt_family="L1" repeat_region /rpt_family="L1" repeat_region /rpt_family="ALU" repeat_region /rpt_family="ALU" repeat_region /rpt_family="L1" repeat_region /rpt_family="L1" /rpt_family="L1" /rpt_family="L1"	repeat_region 44559 .4954 repeat_region 45422 .45448 repeat_region 7.pt_family="hl" repeat_region complement(45615 .4569) /rpt_family="hl" repeat_region from to the family fa	repeat_region /4837046785 /rpt_family="11" repeat_region complement(4957750216) /rpt_family="11" repeat_region complement(5054050791) /rpt_family="THE" repeat_region /rpt_family="THE" repeat_region /rpt_family="THE" repeat_region /rpt_family="The" repeat_region /rpt_family="11" repeat_region /rpt_family="11" repeat_region /rpt_family="11" /rpt_family="11" /rpt_family="11" /rpt_family="11" /rpt_family="11" /rpt_family="11"	repeat_region complement(5176552058) /rPt_family="ALU" repeat_region complement(522552467) Query Match Best Local Similarity 100.0%; Pred. No. 2.4e-229; Matches 405; Conservative 0; Mismatches 0; Indels Qy ggtcactgtaggtgtgattggaagtggagattttgccaaatccttgaccattc-	175 1 175 176	Oy 241 taaaatcctgattgatgtgagcaataacatgaggataaaccagtacccagaat.
repeat_region complement(1201012299) /rpt_family="ALU" repeat_region /rpt_family="L1" repeat_region /rpt_family="L1" repeat_region /rpt_family="L1" misc_feature 1389714096 repeat_region /rpt_family="L1" misc_feature 157515767 misc_feature 1943619497 //note="similar to human EST 702878 (NID:g314119)" //note="similar to human EST AA123941 (NID:g1682616)	misc_feature mq22169.r1" repeat_region replant repeat_region replant repeat_region replant repeat_region replant repeat_region rept_family="Li" repeat_region rept_family="Lamily=	AA149579 N52554 (N W32120 (N	Notee"similar to human EST N59831 (NID:g1203721) Y=77a10.s1" Y=77a	yf26d05.rl" complement(29587. 29853) /note="similar to human EST R09227 (NID:97611) yf26d05.sl" 3014630314 /note="similar to human EST N78042 (NID:91240) yv71e06.rl" complement(3117031350) /note="similar to human EST N58451 (NID:91202) yv71e06.sl"	repeat_region 197032006 repeat_region 32633263 repeat_region 326332663 repeat_region 7rpt_family="ALU" repeat_region 365836709 repeat_region 365836709 repeat_region 7rpt_family="ALU" repeat_region 7rpt_family="ALU" repeat_region 7rpt_family="ALU" repeat_region 7rpt_family="ALU" /rpt_family="ALU" repeat_region 7rpt_family="ALU"

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/rpt_family="LI"
complement(45672 ..45963)
/rpt_family="LI"
complement(45672 ..45963)
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/rpt_family" ALU.
complement(51721. .51764)
/rpt_family" Ll.
complement(51765. .52058)
/rpt_family" ALU"
complement(52252. .52467)
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complement(50820...
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/rpt_family="Il"
51405...51691
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/rpt_family="L1"
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/rpt_family="L1"
42348. 42409
/rpt_family="L1"
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ASRQVYICSNNIQARQOVIELAROLINFIPIDLGSLSSAREIBULPLINFURGEVVY
AISLAFFELYSFVRDVIHPYARNQSDFYKLPIETVNKTLEIVATTLLSLYYLAGLL
AAAYQLYYGTKYRRFPWHLETWHQCROGLISFFAWNYAYSLCLEDRRSBEYLFL
NMAYQQVHANIENSHWEEWYR IBKYISFGTHSLGLLAYTSIESYSNALHERWEFS
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DLRHLLVGKILIDVSNNMRINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKD
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human BAC clone RG016J04 from 7q21, complete sequence.
AC002064
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Gattung, S. and Maggi, L.
The sequence of H. sapiens BAC clone RG016J04
Unpublished (1997)
/note="unnamed protein product"
                                                                                                                                                                                                                                                   100.0%; Score 493; DB 6;
100.0%; Pred. No. 6e-282;
ive 0; Mismatches 0
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Best Local
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send an E-mail to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 978SK. For references see: Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                           all regions were double stranded or sequenced with an alternate chemistry an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of H_RG016J04;
actual end is at 156214 of H_RG016J04. The orientation of this
clone is unknown.
                                                                                                                                                                                                                                                                                                                                                                                      otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone contains STS sWSS2784 (NID:gll13580) and sWSS893 (NID:g454733).
                                                                                                                              Washington University
                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless
                                                                                                                                                                                                     e-mail: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. 156214
Cycyanism="Homo sapiens"
(db.xref="taxon:9606"
/chromosome="7"
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                                                                                                                         Department of Genetics, Wash
St. Louis, MO 63108, USA
http://genome.wustl.edu/gsc
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2 (bases 1 to 156214)
Waterston,R.
Direct Submission
Submitted (09-MAY-1997)
Genome Sequencing Center
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/rpt_family="L1"

100.0 2453 6 82.2 156214 9 61.7 162928 2 42.4 444 6	42.4 444 6 AX140724 AX140724 S 42.4 444 6 AX200584 AX200589 S	209 42.4 444 6 Ax267240 Ax267240 Ax267240 Ax2067240 Ax2067240 Sequence 139 28.2 328 6 Ax106722 Ax140722 Sequence 139 28.2 328 6 Ax200582 Sequence 139 28.2 328 6 Ax200582 Sequence	28.2 27.2 172915 18.9 87401 5.7 205085 2	5.7 227144 2 AC092404 4.5 158682 2 AC023083 4.5 169607 2 AC023569	4.5 180573 9 AC027689 4.3 120743 2 AC091397 4.3 128615 9 AL591051	4.3 165686 10 AC090529 4.3 170278 2 AC020586 4.1 42042 3 CEC34B4	4.1 57220 2 AC100359 4.1 70957 2 AP004214 4.1 81398 2 AC023621	4.1 83921 9 AP001255 AP00125 4.1 89131 2 AC106999 AC10699	4.1 93836 9 ACUI6/10 4.1 151164 2 AC109808 4.1 161086 2 AC09/982 4.1 169109 2 AC025277	4.1 174637 2 AC027490 AC02745 4.1 178173 2 AP002414 AP00241 4.1 179497 9 AL355580 AL355580	4.1 179691 9 AC006572 4.1 182975 9 AP003558 4.1 185326 9 AC023600 AC02360	4.1 185619 2 AC095866 AC05666 Rattu AC057247 AC057247 HOMO 4.1 188925 2 AC084833 AC084883 HOMO	4.1 191109 9 AP004249 AP004249 Homo 4.1 205402 2 AL645584 AL645584 Mus ms 4.1 224573 9 AC008758 Homo 4.1 340000 9 AP001686 Homo	ALIGNMENTS	1	AX155249 Sequence 7 f AX155249		<pre>Homo Sapiens Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2453) Afar, D.E., Hubert, R.S., Raitano, A.B., Saffran, D.C., Mitchell, S.C.,</pre>	Faris, M. and Jakobovits, A. Serpentine transmembrane antigens expressed in hu cancers and uses thereof. Patent: WO 0140276-A 7 07-JUN-2001;	Urogenesys, Inc. (US) Location/Qualifiers - 12453	/organism="Homo sapiens" /db_xref="taxon:9606" 3551719
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model 6	Run on: September 20, 2002, 09:50:05; Search time 4356.39 Seconds 7 (without alignments) 9 2368.195 Million cell updates/sec 10		Scoring table: OLIGO_NUC C 15 Gapext 60.0 , Gapext 60.0	hed: 1797656 seqs, 10463268293 residues	Word size : 0 c 21 c 22 Total number of hits satisfying chosen parameters: 3595312 c 22 c 23	O	Post-processing: Listing first 45 summaries	onEmbl:* gb_ba:* gb_htg:*	gb_in;* c gb_on:* c gb_on:*	gb_pat:* gb_ph:* gb_pl:*	gb_pr:* gb_ro:* gb_ro:*	gb_sy:* gb_un:* gb_u1:* cem_ba:*		20: em_om:* 21: em_or:* 22: em_ov:* AX155249	em_pat:* em_ph:* em_pl:*	em_ro:* em_sts:* KE em_un:* S0	23: em_v1:* 30: em_htg_hum:* 31: em_htg_olinv:* 33: em_htg_olinv:* 33: em_htg_olinv:*	results predicted by chance to have a 1 to the score of the result being printed, of the total score distribution.	SUMMARIES FEATURES SOURCES	Result Query No. Score Match Length DB ID CDS

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Pred. No. 7.2;

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Mismatches

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BE964621 1024 bp mRNA linear EST 14-DEC-2000 601658547R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885898 3', mRNA sequence.

BE964621
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1024)
NNIH-MGC http://mgc.nci.nih.gov/
NNIH-MGC http://mgc.nci.nih.gov/
Uppublished (1999)
On Oct 3, 2000 this sequence version replaced gi:10575326.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue_Procurement: DCTD/DPF/Gazal.
                                                                                                       165 TGAAGAGAGAAATTGGAAAA 185
                                                                          173 tgaagagagaaattggaaaa 193
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Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                    A2976237 716 bp DNA linear GSS 27-APR-2001 2M0251P03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0251P03 R, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 716)
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     Gaps
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/db_xref="taxon:10090"
/clone="UGC2MC251P03"
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     Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0251 row: P column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 716.
Location/Qualifiers
  0; Mismatches
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                                              AZ976237.1 GI:13847464
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     Conservative
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801 585 7177
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.n column: 11
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cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Matches 21; Conservative
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DB 12; Length 716;

Score 21;

4.18;

Query Match

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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-E1
library is a subtracted library derived from the UI-R-E0
library. The UI-R-E0 library consisted of a mixture of
individually tagged normalized libraries constructed from
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CDNA Library Preparation: M.B. Soares Lab Clone distribution:

clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at

LLNL (info@tmage.llnl.gov). IMAGE ID- 1780077

Seq primer: M13 Forward.
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Fax: 319 335 9565
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Program for Rat Gene Discovery and Mapping
University of Iowa
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0.00047;
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/db_xref="taxon:10116"
/clone="UI-R-E1-fv-a-01-0-UI"
/clone_lib="UI-R-E1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.6%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 29; Conservative 0; Mismatches
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8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of or aclone within the mixture. The subtracted library (UI-R-EI) was constructed as follows: PCR amplified CDNA inserts from a pool of UI-R-EO clones from which 3' ESTS had been derived was used as a driver in a hybridization with the UI-R-EO library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-EI library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL636393 XGC-neurula Silurana tropicalis cDNA clone TNeu021f08 5',
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/db_xref="taxon:8164"
/clone="Thew021160"
/clone=lib="xcc-neurula"
/dev_stage="neurula"
/lab_host="scherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-woft cut cDNA was then ligated into pCS107 with
EcoRI-woft at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   western clawed frog.
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
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TROPICALIS_SEQUENCE_ID: TNeu021f08.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
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Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
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Location/Qualifiers
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AL636393.1 GI:16788372
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Best Local Similarity 100.4
Matches 25; Conservative
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DB 9; Length 653; 2.1;

4.3%; Score 22; 100.0%; Pred. No.

Query Match Best Local Similarity

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 680)

8 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.

Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda

M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,

Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki

D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Sano, H., Sasaki

Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,

Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

On Dec 5, 2000 this sequence version replaced gi:11555390.

Contact: Yoshinide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9225

Fax: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tzawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,B., Yamanaka,I., Aizawa Hayashizaki,Y.
       EST 26-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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/dev_stage="15 days embryo"
/dev_stage="15 days embryo"
/dev_stage="15 days embryo"
/note="site_1: Salr; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia
BB603988 RIKEN full-length enriched, 15 days embryo head Musmusculus cDNA clone D930007L06 5', mRNA sequence.
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/clone="D930007L06"
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                                                                                                                                       BB603988.2 GI:16450725
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                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                           house mouse
                                                                                                       BB603988
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was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 712)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Welss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A2428664 10SS 03-OCT-200 1MO212F14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0212F14 F, DNA sequence.
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Project of Genome Exploration Research Group in Riken
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                  Length 680;
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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0.00046;
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                                                                                                                                                                                                                                                                                                                                                                                5.6%; Score 29; DB 100.0%; Pred. No. 0.0 tive 0; Mismatches
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Plate: 0212 row: F column: 14
Seq Primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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/db_xref="taxon:10090"
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Best Local Similarity 100..
"Thes 29; Conservative
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Fax: 801 585 7177
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84112, USA
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Score 29; DB 9; Le
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                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 644)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishli,Y., Ito,M., Kawai,J., Konno,H., Kouda Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Sakai,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takabashi,F., Takeda,Y., Tanaka,T., Toya,T., RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIXEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1711 (2000)

(10 (11), 1757-1711 (2000)

(11), 1757-1711 (2000)

(12), 2000, H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo,S., Shinaqawa,A., Saito,T., Kiyosawa,H., Yamanaka,II., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
perpare full-length cDNA libraries for rapid discovery of new
agi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922 Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
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                                                                                                                                                                                                                                                                                                                                                         On Dec 5, 2000 this sequence version replaced gi:11555852. Contact: Yoshihide Hayashizaki
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/lab_host="DH10B"
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/db_xref="taxon:10090"
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COMMENT
                                                                               REFERENCE
                                                                                                            AUTHORS
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FEATURES

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BI105662 677 bp mRNA linear EST 26-JUN-2001
602892429F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5037414 5',
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                                                                                                                                                                                                                 Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musl. 1 (bases 1 to 677)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Stem cell origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Thoryte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.rd column: 07
Plate: LLAMI1103 row: j column: 07
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100.0%; Pred. No. 0.00046;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="CZECH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:5037414"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_Lu29"
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                                                             mRNA sequence.
BI105662
BI105662.1 GI:14556555
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LOCUS DEFINITION

RESULT AI930004

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ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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/note="Organ: kidney; Vector: pWE18S-FL3; Site_1: DraIII (CACTOTGTG); Ist strand cDNA was primed with an oligo(dT) primer is stranded to a no ligo(dT) primer carranted cDNA was primed to a DraII adaptor (TGTTGGCCTATGTG), digested and choned into distinct DraII sites of the pWE18S-FL3 vector (5' site CACTGTGT, 3' site CACCATGT) should be used to isolate the CDNA insert. Size selection was
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                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 541).
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Ritter,Materston,R. and Wilson,R., Cardenas,M., McCann,R., Mulson,R., Mulson,R., Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACTCCAGTTCGAGCAAA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
ul03e11.yl Sugano mouse kidney mkia Mus musculus cDNA clone MAGE:2055004 5', mRNA sequence.
AI747886
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/organism="Muss musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="InAGE:2065004"
/clone=lib="Sugano mouse kidney mkia"
/sex="female"
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High quality sequence stop: 498.
Location/Qualifiers
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                                                                                   506 bp mRNA linear EST 30-JUL-1999 ulf60d05.y1 Sugano mouse kidney mkia Mus musculus cDNA clone A1930004 a1930004
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Ritter Waterston, R. and Wilson, R.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:999629
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Other_ESTs: ul60d05.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/clone="IMAGE:2123433"
/clone_lib="sugano mouse kidney mkia"
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333 ATCTCTATGATGGGAAGCCCTAAGAGCCT 361
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/dev_stage="adult"
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Fax: 314 286 1810
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source

FEATURES

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Gaps

Query Match

RESULT AI747886

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LOCUS

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BASE COUNT ORIGIN

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Email: genome-res@gsc.riken.go.jp,
URL:http://genome-res@gsc.riken.go.jp,
Carinol.P., Shibata,Y., Hayatsu, Sugahara,Y., Shibata,K., Itoh
Carinol.P., Shibata,Y., Hayatsu, M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKRN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                             Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii,
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Tayahashi, K., Matahiki, A., Matahiki, A., Matahiki, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAS (Akimura, T., et al.
                                                                                            BB862648 RIKEN full-length enriched, kidney CCL-142 RAG CDNA Mus musculus CDNA clone G430029C07 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-72. Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                    EST 26-NOV-2001
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URL: http://genome.gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
M., Konno,H., Okazaki,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length.cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yonedda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                           BB859054 RIKEN full-length enriched, bladder RCB-0544 MBT-2 cDNA Mus musculus cDNA clone G430005B15 5', mRNA sequence.
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                                    linear
                                    mRNA
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/cell_line="RCB-0544 MBT-2"
108 c 141 q 91 t
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BB859054
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/clone_lib="RIKEN full-length enriched, kidney CCL-142 RAG
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Pred. No. 0.00042;
0; Mismatches 0; Indels
                                                    /tissue_type="kidney"
/cell_line="CCL-142 RAG"
127 c 149 g 9
/db_xref="taxon:10090"
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             /clone="G430029C07
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100.0%; Pre
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                                                      /note="Organ: lung_tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal: A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
100 c 99 g 140 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Commercial broiler chickens"
/db_xref="taxon:9031"
/clone="tayon:pk005.18"
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Pituitary/Hypothalamus/Pineal Library (pgp2n)"
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/dev_stage="Embryonic (d12,d14,d19); post-hatch (1,3,5,7,9)
weeks)"
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153 c 144 g 126 t
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Gallus gallus

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

I (bases 1 to 573)

Porter,T.E. and Cogburn,L.A.

ESTS from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA

library, USDA/IFAFS Animal Genome Project

Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                Gaps
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100.0%; Pred. No. 1.1e-06;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                   Query Match
9.1%; Score 47; DB 10; I
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
TEL: 302-831-1332
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
BM491178
BM491178.1 GI:18612109
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM491178
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/Glone="Indexon:10090"
/clone="Inbe"Sugano mouse kidney mkia"
/clone_lib="Sugano mouse kidney mkia"
/clone_lib="Sugano mouse kidney mkia"
/dev_stage="adult"
/lab_host="DH10B"
/dev_Stage="adult"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pME185-FL3; Site_1: DraIII
(CACTGTGTG): Site_2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
|ATGTGGCCTTATTTTTTTTTT]; double-stranded cDNA was
|ATGTGGCCTTATTTTTTTTT]; double-stranded cDNA was
|ligated to a DraIII adaptor [TGTTGGCTAGTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). KhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTGTGCTGTAAAAGCTGCG and 3' end
primer GACCTGCAGCTGGAAGCACA."
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
El (Chases I to 379)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylle, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, F., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.,
Unpublished (1999)
Other ESTs: ul63b08 x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
Wathington Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                         EST 30-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
ul63b08.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2123703 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·:
0
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100.0%; Pred. No. 0.0004;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .379
/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 atctctatgatgggaagccctaagagcct 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: custom primer used.
Location/Qualifiers
1. .379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 ATCTCTATGATGGGAAGCCCTAAGAGCCT 151
                                                                                                                                                               AI930312.1 GI:5666276
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RESULT

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Gaps

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Best Local Similarity 100. Matches 34; Conservative

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3.9 481 9 BE211893 3.9 542 12 AQ619497 3.9 556 10 BF422234 3.9 628 10 BJ119688	20 3.9 888 9 AL544078 AL544078	3.7 409 12 BH066457 3.7 412 10 H30846 3.7 430 9 AA121811 3.7 470 12 AZ519781 3.7 520 10 BF644068 3.7 5.40 10 BF646068	3.7 550 12 BH262095 3.7 560 9 BE207123 3.7 568 10 BF648975 3.7 568 10 BF648975	3.7 575 10 BEGJOOG 3.7 575 40 AJ88959 3.7 606 12 AQ688110 3.7 616 10 BI548782	3.7 649 10 BF650078 3.7 654 10 BF640382 3.7 662 10 BG448710	3.7 664 10 BF645351 3.7 675 10 BI264449	ALIGNMENTS	BF883142 QV3-2F0211-071200-529-b10 ET0211 Homo sapiens CDNA, mRNA sequence.	Br683142,1 GI:12273268 BST. human.	Homo sapiens Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 483)	Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and	Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	cad. Sci.	Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,	Brazil: +55-11-2704922 Fax: +55-11-2707001 Fax: +55-11-2707001 Fax: +55-11-2707001 Figure 2	Location/Quantiters 1483 /organism="Homo sapiens"
C 108	0 0 0 23 24 25 25 25 25 25 25 25 25 25 25 25 25 25	28 28 23 23 23 23 23	0 00 3 8 6 3 6 7 5		0 41			- U Z		ORGANISM * * * * * * * * * * * * * * * * * * *	ir	TITLE	JOURNAL MEDLINE		S G G G	rce
4.5 Compugen Ltd.	; Search time 5053.42 Seconds (without alignments) 1380.832 Million cell updates/sec	.aatcctaagttggcttctga 517	·	27472414							to have a being printed,		Description	BF883142 QV3-ET021 BM491178 pgp2n.pk0 A1930312 u163b08.y	BBB59054 BBB59054 BBB62648 BBB62648 A1930004 u160d05.y A1747886 u103e11.y BB604450 B1105662 602892429 BB60398 BB603988 A2428664 1M0212F14 BF560333 U1-F-E1-f AL636393 AL636393 BB506333 AL6363539	BE504021 0010J0J4/ BG283322 602407051 BE213064 IpBrn0131
×	čea O th	aat	residues	 ຫ							results predicted by chance to have I to the score of the result being prof the total score distribution.		Ω		8 B B B B B B B B B B B B B B B B B B B	

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; LOCATION: 1..4707 US-09-459-066-1

0; Gaps Query Match 3.3%; Score 17; DB 4; Length 4707; Best Local Similarity 100.0%; Pred. No. 15; Matches 17; Conservative 0; Mismatches 0; Indels

; 0

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Search completed: September 20, 2002, 09:49:23 Job time: 11751 sec

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0
                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 4707;
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1. Application US/09459066

Patent No. 6187909

GENERAL INFORMATION

TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN

TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Janis C. Henry

STREET: 51 University St.

CITY: Seattle

STATE: WA

COUNTRY: WA

STATE: WA

STATE: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.3%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 15; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                               LOCATION: 1..4707
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,066
  TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE:
                                                                                    LENGTH: 4707 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISCRATION NUMBER: 34,347
REFERENCE/COCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 999c9c999999c9c99 166
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LENGTH: 4707 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 GGGCGCGGGGGCGCG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-459-066-1/c
                                                                                                                                                                                                                                                                                                                           US-09-458-791-1
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0
                                                         CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING DATE: October 26, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.3%; Score 17; DB 3; Length 4707;
100.0%; Pred. No. 15;
1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-09-458-791-1/C
; Sequence 1, Application US/09458791
; Patent No. 6174689
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VECEPTOR DNA AND POLYPEPTIDES
APPLICATION NUMBER: US 08/958,598 (converted to a APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/458,791
FILING DATE: 10-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
RAPLICATION NUMBER: 08/958,598
FILING DATE: 28-007-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206,470-4189
TELEPAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4707 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 99909099999999 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: 1..4707
US-09-181-706-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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APPLICANT: Barr, Philip J

APPLICANT: Barr, Philip J

APPLICANT: Hicher, Michael C

TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and

TITLE OF INVENTION: Compositions in Cells

FILE REPERENCE: CHIR-009/04US

CURRENT FILING DATE: 1999-01-25

EARLIER APPLICATION NUMBER: 08/447,642

EARLIER PILING DATE: 1999-02-3

EARLIER PILING DATE: 1999-02

EARLIER PILING DATE: 1994-08-02

EARLIER PILING DATE: 1994-08-02

EARLIER PILING DATE: 1992-03-09

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PATENTIN Ver. 2.0
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APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.3%; Score 17; DB 4; Length 4403; 100.0%; Pred. No. 15; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                 Length 4403;
                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                             Score 17; DB 2;
Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
PCT-US93-02147A-1
; Sequence 1, Application PC/TUS9302147A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09236503
Patent No. 6277590
                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                   LENGTH: 4403 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                           150 999c9c999999c9c99 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 gggcgcgggggggcggg 260
                                                                                                                                                                                                                                                               Query Match 3.3°
Best Local Similarity 100°.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.3
Best Local Similarity 100.
Matches 17; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                            NAME/KEY: CDS
; LOCATION: 170..3077
US-08-447-642-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (170)..(3076)
US-09-236-503-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                         TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4403
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-236-503-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Melanie K. Spriggs, Michael R. Comeau, APPLICANT: Robert F. DuBose, Richard S. Johnson TITLE OF INVENTION: VIRAL ENCODED SEWAPHORIN PROTEIN TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES CORRESPONDENCE ADDRESS:
                                                                                 COMPUTER: IBM PC COMPAILLLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02147A
FILING DATE: 19930309
CLASSIFICATION NUMBER: US 07/848,629
FILING DATE: 09-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NELLEY PH.D., RICHARD L
REGISTRATION NUMBER: 30092
REGISTRATION NUMBER: 30092
REGISTRATION NUMBER: 30092
REGISTRATION NUMBER: CHIR-009/00US
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELEFRANC (415) 494-7623
TELEFRANC (415) 494-7623
TELEFRANC (415) 487-7623
TELEFRANC (415) 494-7623
TELEFRANC (415) 487-7623
TELEFRANC (415) 487-7623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17; DB 5;
Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.3%; Sco.
100.0%; Pre
0;
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                                                    E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Janis C. Henry STREET: 51 University St. CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 4403 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 gggcgcggggggcgg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 GGGCGCGGGGCGCGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (CDNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170..3077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
USA
                94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US93-02147A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
COUNTRY:
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APPLICANT: BARR, PHILIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
CORRESPONDENCE: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 4403;
15;
          SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,941
FILING DATE: 2 August 1994
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: NEELEY H.D. RICHARD L.
REGISTRATION NUMBER: 30092
REFERENCE/POCKET UNMBER: 30092
REFERENCE/COCKET UNMBER: 37092
RELEERAX: (415) 843-5070
TELEFRAX: (415) 843-5070
TELEFRAX: (415) 843-5070
TELEERAX: (415) 857-0663
TELEY ARONG SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: ALOUS DASE PAIRS
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FIVE PALO ALTO SQUARE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: THE PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,642
FILING DATE: 23-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/284,941
FILING DATE: 2 August 1994
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L.
REGISTRATION NUMBER: 30092
REFERENCE/POCKET NUMBER: 30092
TELECOMMUNICATION INDERS: 30092
TELECOMMUNICATION INDERS: 30093
TELECOMMUNICATION INDERS: 30093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.3%; Score 17; 100.0%; Pred. No.
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08447642
Patent No. 5989890
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 843-5070
TELEFAX: (415) 857-0663
TELEX: 380816 COOLEY PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 gggcgcggggggcgcgg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 GGGCGCGGGGCGCGG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0
Matches 17; Conservative
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170..3077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY;
; LOCATION:
US-08-284-941-1
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                              Sequence 10, Application US/08840204

Patent No. 6103498

GENERAL INFORMATION:
APPLICANT: LAWRENCE, DANIEL A.
APPLICANT: STEFANSSON, STEINGRIMUR P.
TITLE OF INVENTION: MUTANT PLASMINGEN ACTIVATOR-INHIBITOR
TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMARISON & FOERSER
STREET: Z000 PENNSYLVANIA AVENUE, NW
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: Z0006-18812
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Patent No. 5863756
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GOWARD CASTRO HUDDLESON & TATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17; DB 3; Length 2876;
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                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.3%; Score .,,
100.0%; Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: LIVNAT, SHWUEL
REGISTATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 30807
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEERA: (202) 822-0168
TELEX: 90-4030 MRCNFOERSWSH
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTE READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2876 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 gggcgcggggggcgcgg 166
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Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
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STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-284-941-1
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Gaps

Gaps

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APPLICANT: LAWRENCE, DANIEL A.
APPLICANT: STEFANSSON, STEINGRIMUR P.
TITLE OF INVENTION: MUTANT PLASMINGEN ACTIVATOR-INHIBITOR
TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
TOWNER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2876;
                                                                                 Query Match 3.3%; Score 17; DB 1; Length 650; Best Local Similarity 100.0%; Pred. No. 15; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORINY/AGENT INFORMATION:
NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REPERRENCE/COCKET UNBRER: 30807-20004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEFAX: (202) 822-0168
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.3%; Score 17; DB 100.0%; Pred. No. 15; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2000 PENNSYLVANIA AVENUE, NW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                US-08-840-204-1/c; Sequence 1, Application US/08840204; Patent No. 6103498
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                                                                                                                                                                                               466 GGCGCGGGGGCCCGG 450
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LENGTH: 2876 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.3
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                        US-08-645-865-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-840-204-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08645865
Patent No. 5654406
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: BEBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
.CORRESPONDENCE ADDRESS:
ADDRESSE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
CLASSIPICATION: 435
ATTORNEY ACCURATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 15;
Mismatches
                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTATION NUMBER: 34,438
REFERENCE/DOCKET NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
TELEFAN: 404-688-0770
TELEFAN: 404-688-980
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 base pairs
TYPE: nucleic acid
STRANDENNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1414.608
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Best Local Similarity 100.0%; P;
Matches 17; Conservative 0;
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NAME: PERFYMAN, DAVID G
RECISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  466 GGCCCGGGGCCCCG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 gggcgcggggggcgcgg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 650 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               404-688-9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-08-229-515A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-645-865-13/c
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Gaps

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US-09-167-354-5

Sequence 5, Application US/09167354A

Sequence 5, Application US/09167354A

Patent No. 618659

GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Extander, Mark

APPLICANT: Pyati, Jayashree

APPLICANT: HUVAR, Arne

TITLE OF INVENTION: SUBTYPE

TITLE OF INVENTION: SUBTYPE

TITLE OF INVENTION: SUBTYPE

CURRENT APPLICATION NUMBER: US/09/167,354A

CURRENT APPLICATION NUMBER: US/09/167,354A

CURRENT PILING DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                             3.7%; Score 19; DB 3; Length 2689;
100.0%; Pred. No. 1.4;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.7%; Score 19; DB 3; Length 2699;
100.0%; Pred. No. 1.4;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/08229515A
Patent No. 5518885
GENERAL INFORMATION:
APPLICANT: RAZIUDDIN
APPLICANT: RAZIUD H
TITLE OF INVENTION: BEBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
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CORRESSPONDEMES ADDRESSES
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Accordia
COUNTRY: usa
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                       SEQUENCE CHARACTERISTICS:
LENGTH: 2689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity 100.
Matches 19; Conservative
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291..1625
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Best Local Similarity
Matches 19; Conserv
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; LOCATION:
US-09-165-543-1
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LENGTH: 2699
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Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.7%; Score 19; DB 2; Length 2689;
100.0%; Pred. No. 1.4;
Live 0; Mismatches 0; Indels
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ZIP: 02109
MEDIUM TYPE: FLORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREWY APPLICATION DATR:
APPLICATION NUMBER: US/09/165,543
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
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NAME: Elizabeth A. Hanley
REGIGSTRATION NUMBER: 33,505
REFRENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                   ATTORNEY CACHT INFORMATION:
NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOOKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
TELEPAN: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 19; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COUNTRY: USA
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; LOCATION: 291..1625
US-08-985-090-1
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Sequence 1, Appli
Sequence 129, App
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APPLICANT: Pyati, Jayashree
APPLICANT: Huvar, Arne
TITLE OF INVENTION: SUBTYPE
TITLE OF INVENTION: SUBTYPE
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 375
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TITLE OF INVENTION: MSCARINIC RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
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US-08-750-458A-1

US-08-968-542C-1

US-08-460-751-1

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US-08-658-136-4

US-08-552-874-1

US-09-096-942-2

US-09-096-942-2

US-09-096-867-2

US-08-136-1

US-08-136-1

US-08-658-136-1

US-08-997-362-129

US-08-997-362-129

US-08-997-362-129

US-09-095-855-129

US-09-333-977-11
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Pred. No. 1.4;
0; Mismatches
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; Sequence 8, Application US/09167354A
; Patent No. 6136559
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100.0%; Pre
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ORGANISM: Artificial Sequence
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APPLICANT: Lovenberg, Timothy
APPLICANT: Erlander, Mark
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Best Local Similarity 100.
Matches 19; Conservative
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Massachusetts
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COMPUTER READABLE FORM:
     USA
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STATE: Ma
COUNTRY:
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US-08-985-090-1
     FEATURE:
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Compugen Ltd
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US-08-869-506-1
US-09-128-967-1
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                  GenCore version
Copyright (c) 1993 - 2000
                                                                                         - nucleic search, using sw model
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length: 2000000000
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                                                                                      Query Match 34.4%; Score 178; DB 23; Length 2192; Best Local Similarity 99.6%; Pred. No. 6.3e-85; Matches 228; Conservative 0; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumnours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; human; breast disease; breast cancer; development disorder; ss;
Probe #4411 used to measure gene expression in human breast sample.
                                                                                                                                                   Sequence 1953 BP; 633 A; 316 C; 324 G; 680 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID No 4411; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                         AAI04420 standard; DNA; 1953
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                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                  AAI04420;
                      103
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NAMES OF COLOR OF STREET STREE

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Gaps

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34.4%; Score 178; DB 22; Length 1953; 99.6%; Pred. No. 6.3e-85; ive 0; Mismatches 1; Indels 0;

Query Match 34.4 Best Local Similarity 99.6 Matches 228; Conservative

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colypmerase chair reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques correstore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical maging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical clisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human call diagnostic coding sequences of the invention.
459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                        ggaaggtcactgtaggtgtgattggaagtggagattttgccaaatccttgaccattcgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #12297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 12297; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                           AAS76493 standard; cDNA; 2192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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462

ВР

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460 ttattagatgcggctatcatgtggtcataggaagtagaatcctaagtt 508
                                                                                                           AAI35978 standard; DNA; 1953
                                                                                                                                                                                                        17-0CT-2001
                                                                                                                                                                                      AAI35978;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                        in human cervical cell sample.
                    462
                                      ggaaggtcactgtaggtgtgattggaagtggagattttgccaaatccttgaccattcgac 459
                                                gocotaagagoottagtgaaacttgtttacotaatggcataaatggtatoaaagatgcaa 399
           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                          Probe; human; microarray; gene expression; cervical epithelial
                                                                           Sequence 1953 BP; 633 A; 316 C; 324 G; 680 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                        for gene expression analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID No 4539; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank DR;
                                                                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
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2000US-0234687.
2000US-0236359.
                                                                                                                                               AAI14606 standard; DNA; 1953
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2000US-0608408
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                                                                                                                                                                                                                                      cervical cancer; ss
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                     12-0CT-2001
                                                                                                                                                                                                       Probe #4539
                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                 AA114606;
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340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gccctaagagccttagtgaaacttgtttacctaatggcataaatggtatcaaagatgcaa 399
                                     used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome-derived single exon nucleic acid probes useful zing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                          human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1953 BP; 633 A; 316 C; 324 G; 680 T; 0 other;
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Pred. No. 6.3e-85;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID No 4664; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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99.6%;
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                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00663
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                              genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488897/53
                                                                            microarray;
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Matches 228; Conserv
                                                                                                                                                                    WO200157272-A2.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                   Homo sapiens.
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04-OCT-2000;
                                     Probe #4664
                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analyzing
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                                                                            Probe;
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Length 1953;

; DB 22; 6.3e-85;

Score 178; DB Pred. No. 6.3e-0; Mismatches

Match 34.4%; Local Similarity 99.6%; les 228; Conservative

Query Match Best Loca Matches

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ggaaggtcactgtaggtgtgattggaagtggagattttgccaaatccttgaccattcgac

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463 ggaaggtcactgtaggtgtgattggaagtggagattttgccaaatccttgaccattcgac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probes which are derived from genomic sequences expressed in the human brain. Call samples, brain. They can be used to measure gene expression in brain call samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and cancers. The present sequence is one of the probes of the
                     present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                     Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon nucleic acid probes for analyzing gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 4505; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                 Human brain expressed single exon probe SEQ ID NO: 4505.
                                                                                                        633 A; 316 C; 324 G; 680 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                    AAK04514 standard; DNA; 1953
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2000US-0608408.
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                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                          epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                                                                                                                                                                   WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1953
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27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
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                                                                                                                                                                                                        AAK04514;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                gene expression analysis; probe;
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                                                                                                             Human bone marrow expressed single exon probe SEQ ID NO: 4573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes useful
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                                                                                                                                                                    cancer; leukaemia; lymphoma; myeloma; ss.
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Pred. No. 6.3e-85;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid panalyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank
                                                                                                                                                  Human; bone marrow expressed exon;
 BP
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2000US-0632366.
2000US-0234687.
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ilarity 99.6%;
Conservative (
standard; DNA; 1953
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2000US-0207456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0236359
                                                                        (first entry)
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                                                                                                                                                                                                                                          WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                         Homo sapiens.
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26-MAY-2000;
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04-OCT-2000;
                                                                        06-NOV-2001
                                                                                                                                                                      microarray;
                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probes
AAK30016
                                     AAK30016;
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Best Local S
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6

Gaps

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/ Match 34.4%; Score 178; DB 22; Length 1953; Local Similarity 99.6%; Pred. No. 6.3e-85; Hose 228; Conservative 0; Mismatches 1; Indels 0;

Query Match

Best Loc Matches

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Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                 Claim 1; SEQ ID NO 4640; 639pp + sequence listing; English.
                                                                                                                                                                                                                      Human foetal liver single exon nucleic acid probe #4640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1953 BP; 633 A; 316 C; 324 G; 680 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank DR;
                                                                                                                                               ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                            ABA56335 standard; DNA; 1953
                                                                                                                                                                                                                                                                                                                                                                                  2000US-0180312.
2000US-0207456.
2000US-0608408.
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                                                                                                                                                                                                                                                                                                      WO200157277-A2
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                01-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human hearts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                     Probe #4442 for gene expression analysis in human heart cell sample.
                                                                                                                                  Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1953 BP; 633 A; 316 C; 324 G; 680 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.4%; Score 178; DB 22; 99.6%; Pred. No. 6.3e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 4442; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                  cardiovascular disease; hyper
congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                               2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
            ABA25976 standard; DNA; 1953
                                                                                                                                                                                                                                                                                                                                                                                                           2000GB-0024263
                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00666
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                           WO200157274-A2
                                                                                                                                                                                                                                                                                                                               26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                Homo sapiens
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                                          ABA25976;
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ABA25976
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1; Indels

Score 178; DB 22; Pred. No. 6.3e-85; 0; Mismatches 1;

34.48; 99.68;

228; Conservative

Matches

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Local Similarity

Query Match

Length 1953;

BP.

ABA45820 standard; DNA; 1953

ABA45820

(first entry)

01-FEB-2002

ABA45820;

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testis-specific polypeptides and the nucleic acids encoding them.

Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the proteins, and included are vectors and host cells expressing the proteins, a transgenic animal expressing the proteins, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to disgnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign of the testis or prostate prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence represents the open reading frame of a prostate present sequence represents the open reading frame of a prostate specific protein, Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 gccctaagagccttagtgaaacttgtttacctaatggcataaatggtatcaaagatgcaa 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 gocotaagagoottagtgaaacttgtttacotaatggcataaatggtatcaaagatgcaa 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Llarity 100.0%; Pred. No. 3.5e-112;
Conservative 0; Mismatches 0;
                      liver cancer; lung cancer; cytostatic; ss
                                                                                                   Location/Qualifiers
178..1650
                                                                                                                                                         /product= "STMP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Fig 4D; 114pp; English.
                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09410.
                                                                                                                                                                                                                                                                                                               24-MAR-2000; 2000US-191929P.
                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                       (SAAT/) SAATCIOGLU F.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-662926/76.
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Best Local Similarity
Matches 229; Conserv
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                                                                                                                                                                                                  WO200172962-A2
                                                                                                                                                                                                                                                                                                                                                                                             Saatcloglu F;
                                                              sapiens
                                                                                                                                                                                                                                      04-OCT-2001
                                                              Homo
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and Br 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                    Human; microarray; single exon probe; gene expression; breast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 4515; 327pp + sequence listing; English
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                                                                   Human breast cell single exon nucleic acid probe #4515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1953 BP; 633 A; 316 C; 324 G; 680 T; 0 other;
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Pred. No. 6.3e-85;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                  2000US-0180312.
2000US-0207456.
2000US-0608408.
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2000US-0234687.
2000US-0236359.
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99.68;
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                                                                                                                                                                                                                                                                                                                                                                                       2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-496933/54.
                                                                                                                      disease; cancer; ss.
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Matches 228; Conserv
                                                                                                                                                                                   WO200157271-A2.
                                                                                                                                                     Homo sapiens.
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21-SEP-2000;
27-SEP-2000;
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30-JUN-2000;
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263 ggaaggtcactgtaggtgtgattggaagtggagattttgccaaatccttgaccattcgac 322

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06-DEC-2000; 2000WO-US33040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Human six transmembrane epithelial antigen of prostate-2 clone GTD3 cDNA.
              рę
                                             present sequence encodes prostate specific protéin, Six-Transmembrane Protein of Prostate 1, STMP1, ORF3.
                                                                                                                                                         Of the prostate (STEAP)-2, alternative version"

of the prostate (STEAP)-2, alternative version"

/note= "CDS does not include start and stop codon"

/transl_except= (pos:1714..172, aa:Asp-Ala)

/transl_except= (pos:1834..1842, aa:Arg-Ser)

/transl_except= (pos:1857..1965, aa:Arg-Ser)

/transl_except= (pos:2050..2050, aa:Arg-Ser)

/transl_except= (pos:2050..2050, aa:Arg-Ser)

/transl_except= (pos:2050..2070, aa:Asn-Phe)

/note= "Inframe stop codon alters the reading frame"
                                                                                                                                                                                                                                                   ggaaggtcactgtaggtgtgattggaagtggagattttgccaaatccttgaccattcgac 459
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Human six transmembrane epithelial antigen
cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer late cancer and lung cancer. The present sequence encodes prostate specific protein, Six-Transmembra
                                                                                                                                                                                                      340 gccctaagagccttagtgaaacttgtttacctaatggcataaatggtatcaaagatgcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-2; STEAP-2; chromosome 7q21; cancer; prostate; colon; bladder; lung; ovarian;
                                                                                                                                       ;
0
                                                                                                                Length 2102;
                                                                                                  Score 229; DB 22; Length LP Pred. No. 3.4e-112;
                                                                                                                                                                                                                                                                                             460 ttattagatgcggctatcatgtggtcataggaagtagaaatcctaagtt 508
                                                                                                                                                                                                                                                                                                        Sequence 2102 BP; 595 A; 424 C; 422 G; 661 T; 0 other;
                                                                                                        44.3%; Scor.
100.0%; Pred. No. 5...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the prostate (STEAP)-2"
709.2073
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/note= "Kozak region"
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                                                                                                             Query Match 44.3
Best Local Similarity 100.
Matches 229; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pancreatic; ss.
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07-JUN-2001

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The present sequence is human six transmembrane epithelial antigen of the prostate (STEAP)-2 clone GTD3 cDNA. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is located on chromosome 7q21 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and parcreatic) expressing STEAP or inhibiting growth or killing cells expresses STEAP, or inhibiting a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expresses administering to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the single chain monoclonal antibody sequence to the cancer cells and the encoded single chain monoclonal antibody is expressed intracellularly.
                                                                                                                                                                                                                                                                           New STEAP (six transmembrane epithelial antigen of the prostate) proteins, expressed in human cancers, useful for detecting and treating
                                                                                                              Faris M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggaaggtcactgtaggtgtgattggaagtggagattttgccaaatccttgaccattcgac
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                                                                                                           Mitchell SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2453;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2453 BP; 648 A; 537 C; 520 G; 748 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.3%; Score 229; DB 22; I 100.0%; Pred. No. 3.4e-112; ive 0; Mismatches 0;
                                                                                                           Saffran DC,
                                                                                                           Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Fig 9A-9D; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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                                                                                                                                                                                                                       P-PSDB; AAE02781, AAE02841.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 229; Conservative
                                                    (UROG-) UROGENESYS INC
                                                                                                           Hubert RS,
                                                                                                                                                                                          WPI; 2001-367804/38
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Best Local Similarity
06-DEC-1999;
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                                                                                                                                        Jakobovits
                                                                                                           Afar DEH,
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Gaps

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Mismatches

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Conservative

Matches 229;

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testis specific polypeptides and the nucleic acids encoding them.
Also included are vectors and host cells expressing the proteins, a
transgenic animal expressing the protein, antibodies against the
proteins, probes for detecting the nucleic acids, antisense molecules
for the nucleic acids and methods of isolating modulators of the
proteins. Compounds that modulate the prostate specific or testis
specific polypeptide are useful to diagnose, prevent or treat disorders
of the testis or prostate particularly prostate cancer, benign
cryptorchidism, undescended, retractile, ascending or vanished
testis. Other proliferative disorders for which the modulators may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence encodes a prostate specific protein, Six-Transmembrane
                                                               prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
                                                         Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer benign prostatic hyperplasia; acute prostaticis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag- b
/note- "Represents 12713 nucleotides of intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note "Represents 1396 nucleotides of intron 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to substantially pure prostate-specific or
                                                                                                                                                                                                                                                                                                                                                                         a
"Represents 338 nucleotides of intron 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= e
/note= "Represents 2372 nucleotides of intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         f
"Represents 2299 nucleotides of intron
Human DNA for Six-Transmembrane Protein of Prostate 1, STMP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1725 BP; 476 A; 340 C; 387 G; 517 T; 5 other;
                                                                                                                                                                                   liver cancer; lung cancer; cytostatic; ds.
                                                                                                                                                                                                                                                                                   Location/Qualifiers
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , cay= c //product= "STMP1" 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09410.
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/note=
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P-PSDB; AAU10187.
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                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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   WKKKKYD BY STAND BY S
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Length 1725;

Score 229; DB 22; Pred. No. 3.4e-112;

Score 229;

44.3%; 5

Best Local Similarity

Query Match

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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer,
                                                                                                                                                                                                                                                                                                                                                                                                               Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ss; ORP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
ggaaggtcactgtaggtgtgattggaagtggagattttgccaaatccttgaccattcgac 459
                            Human cDNA encoding ORF3 of Six-Transmembrane Protein of Prostate 1.
                                                                                                                                                                                                   460 ttattagatgcggctatcatgtggtcataggaagtagaaatcctaagtt 508
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/product= "STMP1, ORF3"
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171..1430
                                                                                                                                                                                                                                                                                            AAS15813 standard; cDNA; 2102 BP
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                                                                                                                                                                                                                                                                                                                                                         16-JAN-2002 (first entry)
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                                                                                                                                                             The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them.

Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The protein services of the protein services of the protein services of the protein protein six-Transmembrane
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                                                                                             prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA encoding Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                  treatment for
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1561;
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1561 BP; 420 A; 319 C; 346 G; 476 T; 0 other;
                                                                                  prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.3%; Score 229; DB 22; 100.0%; Pred. No. 3.4e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. w..
                                                                                polynucleotide for the diagnosis,
                                                                                                                                                                                                                                                                                                                                                                               Protein of Prostate 1, STMP1, ORF2.
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178..1650
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                                                                                                                                     Claim 4; Fig 4H; 114pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 229; Conservative
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                                       WPI; 2001-662926/76
                                                       P-PSDB; AAU10188
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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules of for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be cancer, pancreatic cancer, lava cancer and lung cancer, breast cancer, prostatic cancer, lava cancer and lung cancer. The protein of the cancer and lung cancer. The protein of the cancer and lung cancer. The protein of the cancer and lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids
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/product= "STMP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-662926/76.
P-PSDB; AAU10187.
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Best Local Similarity
Matches 229; Conserv
                                                                     WO200172962-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JAN-2002
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human cDNA encodin	Human cDNA encodin	Human DNA for Six-	Human cDNA encodin	Human six transmem	Human ORF of Six-T	Human breast cell	Human foetal liver	Probe #4442 for de
SUMMARIES	ΙD	AAS15811	AAS15802	AAS15793	AAS15813	AAD07072	AAS15801	ABA45820	ABA56335	ABA25976
	DB:	22	22	22	22	22	22	22	22	22
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                  Gorrell, J. H., Guevara, W., Gorrell, J. Hale, S., Hamilton, K., Gorrell, J. H., Guevara, W., Hart, M., Havlak, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hadgson, A., Hoques, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlson, E., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L. Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Li, Z., Martin, R., Man, J., Maheshwari, M., Mapua, P., Martin, R., Man, J., Marsen, M., Mapua, P., Martin, R., Man, J., Marsey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Miner, Z., Mitchell, T., Mohabbatk, K., Morgan, M., Moura, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Orledo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Pace, A., Payton, B., Peery, J., Perez, L., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Sotherer, S., Sotte, G., Shen, H., Shooshtari, N., Sisson, I., Thomas, S., Usman, K., Vasquez, L., Vera, V., Villalon, B., Peery, J., Tang, H., Tang, H., Tang, H., Tang, H., Stone, H., Svatek, A., Taylor, P., Tamerisa, A., Tamerisa, A., Tamerisa, A., Tang, H., Taylor, B., Wall, Ransey, J., Taylor, C., Taylor, P., Taylor, B., Vera, V., Villalon, B., Wull, R., Wull, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wull, Y., Wull, Y., V., Valla, S., Nelson, D., Weller, R., Wall, R., Wull, Y., Wull, Y., Wull, R., Wu
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Center close name: RPII-1461J7

Sequencing vector: M13; L08821

Chemistry: Dye-primer Bodipy: 21% of reads
Chemistry: Dye-terminator Big Dye: 79% of reads
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 162338 bases at least Q40
Consensus quality: 179527 bases at least Q30
Consensus quality: 170520 bases; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
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NOTE: This is a working draft's sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jan 31, 2002 this sequence version replaced gi:11415074.
Center: Baylor College of Medicine
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Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N.,
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gap of unknown length
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Contact: hgsc-help@bcm.tmc.edu
------- Project Information
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Worley, K.C.
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COMMENT

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HSBBHV3 210 bp DNA linear VRL 02-AUG-1993
Bovine herpesvirus-1 DNA, fusion of left and right genomic termini.
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Specificity of cleavage in replicative-form DNA of bovine
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misc_feature
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AC005079_3
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                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
AC005079_3
WPCOMMENT
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AC069221
                                                                                                                                                                                                     BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 10, 2000 this sequence version replaced gi:9838351.
                                                                                                                                   AC005044 76714 bp DNA linear HTG 10-SEP-2000
Homo sapiens chromosome 7 clone CTB-4N9, WORKING DRAFT SEQUENCE, 5
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 76714)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1206: contig of 1206 bp in length
1306: gap of unknown length
5096: contig of 3790 bp in length
5196: gap of unknown length
10233: contig of 5037 bp in length
10333: gap of unknown length
21866: contig of 11553 bp in length
21866: contig of 11553 bp in length
21966: gap of unknown length
21966: gap of unknown length
                                                                                                                                                                                                                                                                                                                                  The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens'
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----- Genome Center
                                                                                                                                                                                                  AC005044.3 GI:10048126
HTG; HTGS_PHASE1; HTGS_DRAFT
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            2 (bases 1 to 76714)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WUGSC
                                                                                                                                                                   unordered pieces.
                                                                                                                                                                                                                                                      Homo sapiens
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1307
5097
5197
10234
10334
21887
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JOURNAL
REFERENCE
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KEYWORDS
SOURCE
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                                                                                                 RESULT
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/chromosome="7" /clone="CTB-4N9"

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Continuation (4 of 5) of AC005079 from base 300001 (AC005079 Homo sapiens BAC clone C
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 175870)

Nuzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbrooks; S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Blange, K., Blankenburg, K., Bonnin, D.,
Bundy, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Charlstopoulos, C.,
Chen, Z., Chen, Z., Chowdry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., Dayid, R.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H. H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgat, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACU69221 175870 bp DNA linear HrG 31-JAN-2002
Homo sapiens chromosome 3 clone RP11-461J7, WORKING DRAFT SEQUENCE,
19 unordered pieces.
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100.0%; Pred. No. 1.1;
ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                     404 others
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                                                            vector_side:ight"
1307. 5096
//note="assembly_name:Contig20"
5197. 10238
//note="assembly_name:Contig21"
10334. 21886
//note="assembly_name:Contig22"
21987. 76714
//note="assembly_name:Contig22"
a 16021 c 14650 g 22878 t 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 9;
Pred. No. 1.2;
0; Mismatches
                 /note="assembly_name:Contig19
clone_end:SP6
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410000
415268
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100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 tgaaacttgtttacctaatgg 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence split into 5 fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200001
300001
400001
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Matches 21; Conservative
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Best Local Similarity 100.
Matches 21; Conservative
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AC005079_0
AC005079_1
                                                                                            misc_feature
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ACUUDUBS 58780 bp DNA linear HTG 13-MAR-1999
Homo sapiens clone RG302D02, *** SEQUENCING IN PROGRESS ***, 15
unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

Mod 63108, USA

**NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces

**is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

** This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 58780)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                         The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                      AC005085.2 GI:4415964
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 58780)
Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                        Homo sapiens
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10004
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12541
12553
18193
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22056
220103
33076
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36469
36481
38854
38866
44408
47401
47401
47413
53125
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NOTE: This is a "working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                   Submitted (27-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,Y., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Direct Submission

Uppublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 3425 bases at least Q40 Consensus quality: 3888 bases at least Q30 Consensus quality: 4368 bases at least Q30 Estimated insert size: 1226; sum-of-contigs estimation Quality coverage: Ox in Q20 bases; agarose-fp estimation Quality coverage: Ox in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             t
t
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid, N7789 Chemistry: Dye-terminator Big Dye: 92% of reads Assembly program: Phrap; version 0.990329First call findPhrapList
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1859: contig of 876 bp in length
1959: gap of unknown length
3195: gap of unknown length
3198: contig of 1136 bp in length
3788: contig of 593 bp in length
3888: gap of unknown length
5294: contig of 1406 bp in length
5394: contig of 1406 bp in length
6751: contig of 1357 bp in length
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Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6751: contig or 135, re 6851: gap of unknown length 7696: contig of 845 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 883 bp in length
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/db_xref="taxon:10116"
/clone="CH230-151B7"
| 1929 c 1303 g 1932 t
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                                                                                                                                                                 2 (bases 1 to 7696)
Worley, K.C.
Direct Submission
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3789
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6752
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ORIGIN
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AUTHORS
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bp in length

length

bp in length bp in length bp in length

length length length

contig of 2573 b gap of unknown l contig of 2971 b contig of 2231 b gap of unknown l contig of 2231 b gap of unknown l contig of 2525 b gap of unknown l contig of 2525 b gap of unknown l contig of 5640 b gap of unknown l

7799: 10003: 10015: length

of 2573 bp in length

bp in length

of 3381 unknown 2373 unknown

contig gap of contig gap of contig gap of

36468:

33087

36480:

contig of 3963 gap of unknown

gap of

ength.

bp in length bp in length

ot

length length ength

contig of 2981 gap of unknown contig of 5712

47400:

unknown

bp in length bp in length bp in length

length length Length

gap of unknown contig of 7045 unknown

29100:

length

gap of unknown contig of 3839

8192

18204

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                                                                                                                                                                                        Gaps
                                                                                                                                                                                        ;
0
                                                                                                                                                         DB 2; Length 58780;
1.1;
                                                                                                  279 others
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  length
                                                                                                                                                                                       ;
                                                                                                   17900 a 11129 c 11200 g 18272 t
gap of unknown
contig of 5645
                                                                                                                                                           4.1%; Score 21; DB ilarity 100.0%; Pred. No. 1.1 Conservative 0; Mismatches
                                                       /organism="Homo sapiens"
                                                                      /db_xref="taxon:9606"
                             Location/Qualifiers
                                                                                      /clone="RG302D02
              58780:
                                                                                                                                                           Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                  BASE COUNT
ORIGIN
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Gaps

; 0

3584 ATCTCTATGATGGGAAGCCCTAAGA 3608

324 atctctatgatgggaagccctaaga 348

ŏ g

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iap of 100 bp.

contig of 910 bp in length
iap of 100 bp.

contig of 895 bp in length
iap of 100 bp.

contig of 845 bp in length
                                                                                                                                                                                                                                                                                                                                                                         892: gap of 100 bp 1811: contig of 919 bp in length 911: gap of 100 bp 182806: contig of 895 bp in length 906: gap of 100 bp 18781: contig of 878 bp in length 90781: contig of 878 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                            184: gap of 100 bp
44777: contig of 893 bp in length
177: gap of 100 bp
45768: contig of 891 bp in length
168: gap of 100 bp
46761: contig of 893 bp in length
                                                                                                                                                                                                                                                              36940: gap of 100 bp 37822: contig of 882 bp in length 37822: gap of 100 bp 38845: contig of 923 bp in length 38945: gap of 100 bp 38923: contig of 878 bp in length
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61654: contig of 916 bp in length
           112: gap of 100 bp 28919: contig of 907 bp in length 119: gap of 100 bp in length 29933: contig of 914 bp in length
                                                                  p of 100 bp contig of 897 bp in length
                                                                                           31030: gap of 100 bp 31924: contig of 894 bp in length 32024: gap of 100 bp 32902: contig of 878 bp in length
                                                                                                                                                   33002: gap of 100 bp
33890: contig of 888 bp in length
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contig of 852 bp in length
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contig of 950 bp in length
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contig of 893 bp in length
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55769: contig of 887 bp in length
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contig of 879 bp in length
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contig of 897 bp in length
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p of 100 bp
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contig of 926 bp in length
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63664: contig of 884 bp in length
27912: contig of 929 bp in length
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36840:
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47713: cont
          12: gap of 28919: cont
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40792: con
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62680: cont
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49779: con
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35895: con
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46761:
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Rattus.

Libbrooks, S.L., Amaratunge, H.C., Arel. A., Ayele, M., Banks, T., Barbaria, J., Banton, J., Blange, K., Blankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Blange, K., Blankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Blange, K., Brown, M., Eryant, N. P., Burch, P., Burkett, C., Burch, R., Chacko, J., Chavez, D., Chen, R., Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7696 bp DNA linear HTG 27-JAN-2002 Rattus norvegicus clone CH230-151B7, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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100.0%; Pred. No. 0.001;
.ive 0; Mismatches 0; Indels (
                64670: contig of 906 bp in length
164770: gap of 100 bp
17 65666: contig of 896 bp in length
57 65766: gap of 100 bp
187 66736: contig of 870 bp in length
187 66736: gap of 100 bp
187 66736: gap of 100 bp
187 66764: contig of 868 bp in length
                                                                                                                                                                                                                                        67704: gap of 100 bp

68576: contig of 872 bp in length

68676: gap of 100 bp

69701: contig of 925 bp in length

69701: gap of 100 bp

70618: contig of 917 bp in length
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Rattus norvegicus
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Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="assembly_fragment
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26809._.109655
/note="assembly_fragment
                                                               /organism="Mus musculus"
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                                                                                                                                   /db_xref="taxon:10090"
/chromosome="5"
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Location/Qualifiers
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109756. .227144
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AC021898.2 GI:9119282
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Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

the record is updated, the accession number will
                        Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: Project Information
Center project name: L2445
Center clone name: 407_J_8
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1007 11006; gap of 100 bp
11007 11910; contig of 904 bp in length
11911 12010; gap of 100 bp
12011 12924; contig of 914 bp in length
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13330: contig of 906 bp in length
14030; gap of 100 bp
14919: contig of 889 bp in length
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contig of 860 bp in length
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contig of 923 bp in length
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15900: contig of 881 bp in length
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26883: contig of 896 bp
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                  pulse-field-gel
sum-of-contigs
                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                 agarose-fp
Assembly program: Phrap; version 0.990319
Consensus quality: 199516 bases at least Q40
Consensus quality: 200566 bases at least Q30
Consensus quality: 200506 bases at least Q20
Insert size: 197000; agarose-fip
Insert size: 192000; pulse-field-gel
Insert size: 204185; sum-of-contigs
Quality coverage: 9.60x in Q20 bases; pulse-fie
Quality coverage: 9.60x in Q20 bases; sum-of-co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81789: cortig of 19679 bp in length 81889: gap of unknown length 109919: contig of 28030 bp in length 110019: gap of unknown length 153235: contig of 43216 bp in length 15335; gap of unknown length 205085: contig of 31750 bp in length
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4528: gap of unknown length
9553: contig of 5025 bp in length
9653: gap of unknown length
27746: contig of 13093 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22846: gap of unknown length
33954: contig of 11108 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 13777 bp in length gap of unknown length
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/clone_lib="RPCI mouse BAC library 23"
1. .4428
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40716 c 41296 g 61026 t
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4529. .9553
/note="assembly_fragment"
9654. .22746
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/note="assembly_fragment"
34055. .47831
/note="assembly_fragment"
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110020. .153235
/note="assembly_fragment"
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62111. 81789
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81890. 109919
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/note="assembly_fragment
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/db_xref="taxon:10090"
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ORIGIN
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ACU92404

Mus musculus chromosome 5 clone RP23-261D18 strain C57BL6/J,
AC092404
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Gupta, J., Ho, S.-L., Idol, J.R., Karlins, E., Lee-Lin, S.-Q., Legaspi, R., Lim, M., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Snyder, B., Stantripop, S., Thomas, J.W., Thomas, J.W., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (04-JUL-2001) NIH Intramural Sequencing Center, 8717
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 14.02x in Q20 bases; agarose-fp Quality coverage: 12.84x in Q20 bases; pulse-field-gel Quality coverage: 12.73x in Q20 bases; sum-of-contigs
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                                                           .;
0
       Length 205085;
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Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
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26808: gap of unknown length
109655: contig of 82847 bp in length
109755: gap of unknown length
227144: contig of 117389 bp in length.
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                                                           0; Indels
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Insert size: 225000; pulse-field-gel
Insert size: 226944; sum-of-contigs
                                 1.6e-05;
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Contact: nisc_mouse@nhgri.nih.gov
------ Project Information
               DB
                                                                Mismatches
                                                                                                            5.6%; SCOIE ...
100.0%; Pred. No. 1
... 0; Mismatche
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Center clone name: 261D1
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          Query Match
Best Local Similarity 100.0
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
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                                                                                                                                                                                                                                   RESULT 7
AC092404/c
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                                                                                                                                                                                                                                AC099742 172915 bp DNA linear HTG 20-NOV-2001
Papio cynocephalus anubis clone RP41-167P22, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Akhter, N., Ayele, K., Beckstrom-Sternberg, S.W., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Gupta, J., Haphighi, P.,
Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-O.,
Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D.,
Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Abnay, L., H., and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                         Papio cynocephalus anubis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Submitted (20-NOV-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently a consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 130000; agarose-fp
Insert size: 172615; sum-of-contigs
Quality coverage: 12.58x in Q20 bases; agarose-fp
Quality coverage: 9.47x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2438: contig of 2438 bp in length
2538: gap of unknown length
8133: contig of 5595 bp in length
88233: gap of unknown length
10378: contig of 32145 bp in length
10478: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: NIH Intramural Sequencing Center
                                                                                Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                          SEQUENCE, 4 unordered pieces
                                                                                                                                                                                                                                                                                                               AC099742.1 GI:17017546
                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecinae; Papio.
1 (bases 1 to 172915)
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40378:
40478:
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                                                                                                                                                                                                                                                                                                                                                            olive baboon.
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                                                                                                                                                                                                                                                                                                                                                        SOURCE
ORGANISM
                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                          AC099742
                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                 VERSION
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HTG 27-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 205085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-MAR-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Oct 27, 2001 this sequence version replaced 91:7321458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACO26813 205085 bp DNA linear HTG 27-On Mus musculus chromosome 5 clone RP23-119M19 strain C57BL6/J, WORKING DRAFT SEQUENCE, 10 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 gtatcatggaatcaatctctatgatgggaagccctaagagccttagtgaaactt 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.4%; Score 54; DB 2; Length 172915; 100.0%; Pred. No. 7.6e-21; ive 0; Mismatches 0; Indels 0
Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 others
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Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment"
31733 c 32277 g 56096 t
                                                                                                                                                                                                                                                                               2539. 8133
/note="assembly_fragment"
8234. 40378
/note="assembly_fragment
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Center project name: xh
Center clone name: 119M19
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HTG; HTGS_PHASE1; HTGS_DRAFT.
house mouse.
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                                                                                                                                                                                                                                                             vector_side:right"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green, E.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                        40479.
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Best Local Similarity
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       40479
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                                                                                                                                                                                                                                                                                     misc_feature
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	length	
901 bp 906 bp 906 bp 905 bp 905 bp 905 bp 906 bp 906 bp 923 bp		100 bp 10
901: conti 907: conti 907: conti 912: conti 912: conti 92: conti 93: conti 94: conti 94: conti 94: conti 94: conti 94: conti 94: conti 95: conti	003: gap of 8913: oco 103: gap of 99: gap of 109: gap of 109: gap of 1224: gap of 123: gap of 139: gap of 149: gap of 159: gap of 159: gap of 159: gap of 159: gap of 159: gap of 159: gap of 169: gap of 179: gap of	ap of continuous cont
		219393 21939 2

Query Match 19.3%; Score 100; DB 2; Length 87401; Best Local Similarity 100.0%; Pred. No. 4.4e-49; Matches 100; Conservative 0; Mismatches 0; Indels 0 7 4296: gap of 100 bp 1 7815: gap of 100 bp 100 bp 18812: contig of 897 bp in length 8812: gap of 100 bp 100 b 100 bp g of 893 bp in length 100 bp g of 903 bp in length 82: gap of 100 bp 55769: contig of 887 bp in length 69: gap of 100 bp 65736: contig of 867 bp in length 36: gap of 100 bp 57715: contig of 879 bp in length 36: gap of 100 bp 67604: contig of 868 bp in length 684; gap of 100 bp 68576: contig of 872 bp in length 76: gap of 100 bp 113: gap of 100 bp 48729: contig of 916 bp in length 129: gap of 100 bp 49779: contig of 950 bp in length 770: gap of 100 bp 65666: contig of 896 bp in length 66: gap of 100 bp 66636: contig of 870 bp in length in length 80: gap of 100 bp 63664: contig of 884 bp in length 69601: contig of 925 bp in length 69701: gap of 100 bp 70618: contig of 917 bp in length 30 50794: contig of 915 bp in 55894: gap of 100 bp in 51797: contig of 913 bp in 8 51897: gap of 100 bp in 52886: contig of 889 bp in 53879: qap of 100 bp 36841 36940: gap of 100 bp 36941 37822: contig of 882 bp in 37923 37922: gap of 100 bp 37923 38845: contig of 923 bp in 38846 38945: gap of 100 bp 39924 40792: contig of 869 bp in 39924 40792: contig of 869 bp in 40893 41811: contig of 869 bp in 41812 41911: gap of 100 bp 41812 41911: gap of 100 bp 42907 43784: contig of 878 bp in 42807 43784: contig of 878 bp in 43885 44777: contig of 893 bp in 43885 44777: contig of 893 bp in 44878 44877: gap of 100 bp 100 bp of 852 bp 63764: 'gap of 100 bp 64670: contig of 906 bp 10. 37822: contig of 8t. 38422: gap of 8t. 38452: contig of 8t. 38945: cc. 38 379: gap of 54782: contig of 382: gap of 61: gap of 47713: contig 56836: gap of 57715: contig con.
.: gap of 62680: gap of 49779: 57815: 62780: 47813: 54882: 58812: 59829: 64770: 66736: 60738: 68676: 55869: 67704: 61754: 48829 46861 99759 54883 55770 55870 56737 56837 57716 57816 58713 58813 59730 61655 61755 63665 14878 15769 15869 62681 62781 66637 66737 67605 67705

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Gaps

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Sequencing vector: plasmid: n/a: 100% of reads
Sequencing vector: plasmid: n/a: 100% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 161001 bases at least Q40
Consensus quality: 161422 bases at least Q30
Consensus quality: 161562 bases at least Q20
Insert size: 143000; agarose-fp
Insert size: 162428; sun-of-contigs
Quality coverage: 10.76x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center: NIH Intramural Sequencing Center
                                           Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
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/note="assembly_fragment"
36349..66192
/note="assembly_fragment"
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/note="assembly_fragment"
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-120K11"
                                                                                               ----- Project Information
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/note="assembly_fragment
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1. .13922
/note="assembly_fragment
clone_end:T7
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ORIGIN
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DB 2; Length 162928; Query Match 26.9%; Score 139; DB 2; Best Local Similarity 99.5%; Pred. No. 6e-73; Matches 189; Conservative 0; Mismatches

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Gaps

; 0

1; Indels

Db 37913 AGGATATTCTTGGTGATCTTGGAAGTGTCCGTATCATGGAATCTTCTATGATGGGAA 37854 280 aggatattettggtgatettggaagtgteegtateatggaateatetetatgatggaa 339 ð

340 gccctaagagccttagtgaaacttgtttacctaatggcataaatggtatcaaagatgcaa 399 á

be preserved.

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Andron Sapteus Circume Netletains, Control Marting, Contr
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Homo sapiens chromosome 15 clone RP11-407J8 map 15, LOW-PASS
SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 87401)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone RP11-407J8
Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu
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AC021898.2 GI:9119282
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                                                                                                                                                                                                                                                                                                                                                  Db 37733 TTATTAGATG 37724
                                                                                                                                                                                                                                                                        460 ttattagatg 469
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VERSION
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TITLE
JOURNAL
REFERENCE
AUTHORS
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                           27125. .27544
/note="similar to human EST AA151796 (NID:g1720491)
human EST AA151807 (NID:g1720502)
                                                                      complement(27178. .27600)
Ynote="similar to human EST AA149579 (NID:g1720380)
                                                                                                                                          yv36a11.51"
27686. 27856
7note—"similar to human EST W32120 (NID:g1313113)
2D97c08.f1"
27686. 27838
2097b08.f1"
2b97b08.f1"
                                                                                                                                                                                                                                                                                                                     complement(27887. .28143)
/note="similar to human EST N59830 (NID:g1203720)
y277a09.s1"
                                                                                                                                                                                                                                                                                                                                                                   complement(27997. .28144)
/note="similar to human EST W31628 (NID:gl312688)
2b97c08.sl"
                                                                                                                complement(27441. .27890)
/note="similar to human EST N52554 (NID:g1193720)
                                                                                                                                                                                                                                                                                       .28143)
human EST W31561 (NID:g1312680)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30146. .30314
/note="similar to human EST N78042 (NID:g1240743)
yv71e06.r1"
                                                                                                                                                                                                                                             complement(27733. .28143)
/note="similar to human EST N59831 (NID:g1203721)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(31170. .31350)
//octe="similar to human EST N58451 (NID:g1202341)
                                                                                                                                                                                                                                                                                                                                                                                                                      28666. .28972
/note="similar to human EST R09339 (NID:9761262)
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inote="similar to human EST R09227 (NID:9761150)
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31970..32006
/rpt_family="L1"
32263..32563
complement(34737.
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/note="similar to
zb97b08.s1"
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/rpt_family="PTR"
39839. .40125
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complement(41904.
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complement(45615.
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'rpt_family="ALU"
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15422. .45419
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complement(41340.
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16558. 36709
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44659. .449
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27125. .27
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2348. .42
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Den troglodytes

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Eukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Pan.

Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 162928)

RS Akhter, N., Ayele, K., Beckstrom-Sternberg, S. M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighl, P.,

Ho, S.-L., Idol, J. R., Karlins, E., Laric, P., Lee-Lin, S.-O.,

Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D.,

Thomas, J.W., Thomas, P.J., Touchman, J.W.; Tsurgeon, C., Vogt, J.L.,

Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and

Green, B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA linear HTG 12-DEC-2001
WORKING DRAFT SEQUENCE, 6
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Submitted (12-DEC-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 156214;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 178; DB 9;
Pred, No. 7.5e-97;
0; Mismatches 1.
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                                                                                                                                                                                                                                                                                         /rpt_family="ALU"
complement(51721. .51764)
/rpt_family="L1"
complement(51765. .52058)
/rpt_family="ALU"
complement(52252. .52467)
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                                                                                                                                                       .50791)
.46597)
                                                                                                                                                                                                .50985)
                                                                                                                                                                                                                                    .51156)
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                             /rpt_family="L1"
complement(49577.
                                                                                                                                       /rpt_family="L1"
complement(50540.
                                                                                                                                                                            /rpt_family="THE"
complement(50820.
                                                                                                                                                                                                                  /rpt_family="THE"
complement(51124.
        /rpt_family="L1"
46100. .46516
                                                        /rpt_family="L1"
48370. .48785
                                                                                                                                                                                                                                                       /rpt_family="L1"
51405. .51691
                                                                                                                                                                                                                                                                                                                                                                                                                                 34.4%;
99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                              /POCTEDID id="CAC42678.1"
/PDOCTEDID id="CAC42678.1"
/db_xref="GI:14536714"
/db_xref="GI:14536714"
/LIRAISALGION="MESISMMGSPELSETCLPNGINGIKDARKVTVGYIGSGDFAKS
/LIANSLALION="MESISMMGSPELSETCLPNGINGIKDARKTTVVGFIGSTRSYTELINGICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURICATURIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 156214)
Gattung, S. and Maggi, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156214 bp DNA linear PF Human BAC clone RG016J04 from 7q21, complete sequence. AC002064 G1:2076723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 44.3%; Scoré 229; DB 6; Length 24: Local Similarity 100.0%; Pred. No. 2.3e-128; les 229; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence of H. sapiens BAC clone RG016J04
Unpublished (1997)
2 (bases, R. to 156214)
Waterston, R.
/note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              520 g
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Submitted (09-MAY-1997)
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send an E-mail to
                                                                                                                                                                                                                          This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 9788K. For references see: Shizuya et al., Proc. Nall. Acad. Sci. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996).
                                                                                                                                                                                                                                                                                                                                                                          NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of H_RG016J04;
actual end is at 156214 of H_RG016J04. The orientation of this
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19436. 19497
Anote="similar to human EST AA123941 (NID:g1682616)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/map="7q21"
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M19743 Bovine herp
AX34729 Sequence
M69229 Human insul
A3301639 Plasmodiu
M96453 Bovine herp
U30471 Plasmid pSa
Z54206 Bovine herp
AC100658 Mus muscu
Z78015 Caenorhabdi
AJ004801 Bovine he
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AC022848 Homo sapi
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AC079068 Homo sapi
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2453)

Afar, D.E., Hubert, R.S., Raitano, A.B., Saffran, D.C., Mitchell, S.C., Serpentine transmembrane antigens expressed in human prostate Parent: WO 0140276-A 7 07-JUN-2001;

Urogenesys, Inc. (US)
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/db_xref="taxon:9606"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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